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Result
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Listing first 45 summaries
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Low hazard strain
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Human papillomavir
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AAN91603
AA148310
ABA181897
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AAR87087
AAZ89046
AAC23951
AAC3956
ABL16553
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ABV16004
AAS64558
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ABV30275
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ABX12328
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HPV E6/7 region pr
Human cDNA #752 di
Partial nucleotide
HPV11-E6/E7 region
Human nervous syst
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Streptococcus poly
Human prostate exp
Pinus radiata cell
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Human
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Aspergillus fumiga
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Novel cDNA encodin
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ALIGNMENTS

AAQ48541;

AAQ48541 standard; DNA; 20

BP.

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AAQ4851
IID AAQ4
XX AAQ4
XX AAQ4
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XX BYN
XX Hume
XX JP05
PN J
     Disclosure; Page 13; 18pp; Japanese
                                                                                                                                             Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                                                                                                                                                                                                                                                                                          WPI; 1993-277497/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus; HPV; E6; E7; benign; malignant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe;
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RESULT 3
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ID AAS1
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AAQ48565
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                                                              AAS18613 standard;
                                                                                                                                                                   The probe is used to detect benign and/or malignant human papilloma virus. The probe binds to the E6 and/or E7 region of the virus.
                                                                                                                                                                                      Disclosure; Page 15; 18pp; Japanese
                                                                                                                                                                                                                                 WPI; 1993-277497/35.
                                                                                                                                                                                                                                                                                                    JP05192200-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The probe is used to detect benign and/or malignant human papilloma virus. The probe binds to the E6 and/or E7 region of the virus.
      Human papillomavirus; HPV; early gene;
                   Low hazard strain human papillomavirus (HPV) E6, PCR primer.
                                  26-FEB-2002
                                                AAS18613;
                                                                                                                                                      Sequence
                                                                                                                                                                                                           Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                                                                                                                                                                                                                             (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                            20-AUG-1990;
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                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                             Human papilloma
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                                                                                                                                                                                                                                                                                                                                                          22-FEB-1994
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                                                                                                                                                     3 A;
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                                                                                                                                                                                                                                                                                                                              virus; HPV;
                                                              DNA;
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      E6; PCR primer;
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                                                                                                                                                                                                           Matches
      02-OCT-1987;
                                                           Human papilloma
                   30-SEP-1988;
                                 06-APR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a novel method of identifying viral DNA of human papillomavirus (HPV) in cellular material collected from an individual. The method comprises extracting DNA from the cellular material, amplifying the DNA by using a polymerase, and identifying sequences complementary to sequences in the regions E (early genes) e.g. E6 and E7 of the HDV genes is a polymerase of the HDV genes of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E7 of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E7 of the HDV genes is the regions E (early genes) e.g. E6 and E7 of the HDV genes is the regions E7 of the HDV genes is the region E7 of the HDV genes is
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         Human papilloma cellular smear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20
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                                                                                                                                                  Partial nucleotide sequence type 6 (HPV-6).
                                                                                                                                                                                                                                                                                          17-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                            AAN91601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN91601 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOA-) BIOANALISI CENT SUD DI PERSEU SINIBLADO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGCTAATTCGGTGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTAATTCGGTGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 12; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Montis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 3 A; 5 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000IT-M000091.
virus;
benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
              type 6; in situ hybridisation assay, cervical wart; cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floris MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                              (5<sub>′</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                              end) of human papilloma virus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rly genes) e.g. E6 and
The presence of HPV in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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87US-0103979 88WO-US03367

virus.

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RESULT 5
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent is for a rapid in situ hybridisation assay for detecting and typing human papilloma virus (HPV) in non-frozen cellular smears fixed t a support in absence of aldehyde-based crosslinking reagents. The assay comprises: (1) combining nucleic acid in the sample with at least one detectable probe able to hybridise with 1 or more HPV types; and (2) detecting presence or absence of hybrid complexes. Opt. several probes are used, eg one for HPV types 6 and 11, associated with benign warts, and one for types 16, 18, 31, 33 and 35, associated with cervical cancer. The assay can differentiate between HPV types. It is esp. used as a secondary test. The probes can be synthesised or cloned.
                                                                                                                                                                                                                                                                                                                     HPV; polyprotein;
cervical cancer; ;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAT59430 standard; DNA; 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation test for human papilloma virus in cell smears
by reaction with long labelled probe specific for particular
virus types, esp. for examining cervical smears
                                                       Papilloma virus early useful for treating, e
                                                                                                                           Cox JC, Edwards SJ,
Moloney MBH, Webb EA,
                                                                                                                                                                                                  27-JUL-1995;
                                                                                                                                                                                                                        26-JUL-1996;
                                                                                                                                                                                                                                                 13-FEB-1997.
                                                                                                                                                                                                                                                                        WO9705164-A1
                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                      AAT59430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                               Example 1; Page 22-23; 62pp; English.
                                                                                                                                                               ( uggu )
                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROPROBE CORP
                                                                                          1997-145619/13
DB; AAW01808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
                                                                                                                                                                                                                                                                                                                                                      papillomavirus 6b E6/E5a/E4 DNA cassette CSL690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGCTAATTCGGTGCTACCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                              CSL LTD.
UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTAATTCGGTGCTACCTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731 BP; 245 A; 147 C; 159 G; 180 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams
                                                                                                                                                                                                 95AU-0004439
                                                                                                                                                                                                                        96WO-AU00473
                                                                                                                                                                                                                                                                                                                                vaccine; wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                        Ø
                                                                                                                                                                                                                                                                                             type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                           Frazer I,
Williams
                                                     open
e.g. g
                                                                                                                                                                                                                                                                                              6
                                                        n reading frame
genital warts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                condylomata acuminata;
                                                                                                                                      Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.44;
                                                        polyprotein
and cervical
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                                                                                                                                         McMillan
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                                                        constructs
cancer
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DNA construct CSL690 (AAT59430) codes for an E6/E5a/E4 polyprotein (AAW01808), plus C-terminal hexahistidine tag, of human

Matches Query Match Best Local :

Similarity

100.0%;

Score Pred.

N 20

DB 18; 0.47;

Length 1128;

Conservative

. .0;

Mismatches

0;

Indels

0,

0;

Sequence

1128

BP; 359 A; 274 C;

240 G;

255 T; 0 other;

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RESULT 6
AAT59431
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                    DNA construct CSL760 (AAT59431) codes for an E6/E7/E4 polyprotein (AAW01809) of human papillomavirus 6b (HPV6b), plus a C-terminal hexahistidine tag. It was obtd. by separate PCR amplification of the E6, E4 and E7 genes (see also AAT59412-15 and AAT59418-19) of HCV6b and their cloning into vector pSP70. The resulting E6/E7/E4 cassette was incorporated into pGEX-STOP to allow prodn. of the HPV6b polyprotein in E. coll. The E6/E7/E4 DNA construct, or the encoded polypeptide, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating genital warts and cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 papillomavirus 6b (HPV6b). It was obtd. by separate PCR amplification of the E6, E4 and E5a genes (see also AAT59412-17) of HCV6b and their cloning into vector pSP70. The resulting E6/E5a/E4 cassette was incorporated into pGEX-STOP to allow prodn. of the HPV6b polyprotein in E. coli. The E6/E5a/E4 DNA construct, or the encoded polypeptide, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for
                                                                                                                                                                                               Papilloma virus early open reading frame polyprotein useful for treating, e.g. genital warts and cervical
                                                                                                                                                                                                                                                                                              Cox JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPV; polyprotein;
cervical cancer; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus 6b E6/E7/E4 DNA cassette CSL760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT59431 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1107 BP; 337 A; 268 C; 213 G; 289 T; 0 other;
                                                                                                                                                                                                                                         P-PSDB; AAW01809.
                                                                                                                                                                                                                                                       WPI; 1997-145619/13
                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9705164-A1
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                                                                                                                                                                        Example 1; Page 24-25; 62pp; English.
                                                                                                                                                                                                                                                                                 Moloney MBH, Webb
                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1997
                                                                                                                                                                                                                                                                                                                        (CSLC-) CSL LTD.
(UYQU ) UNIV QUI
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                                                                                                                                                                                                                                                                                                                        UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genital warts and
                                                                                                                                                                                                                                                                                              Edwards
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                                                                                                                                                                                                                                                                                                                                                                                           96WO-AU00473
                                                                                                                                                                                                                                                                                SJ,
b EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 6b
                                                                                                                                                                                                                                                                                 Frazer I,
Williams
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                                                                                                                                                                                                                                                                                 Margetts MP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               condylomata acuminata;
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                                                                                                                                                                                                                                                                                               McMillan
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                                                                                                                                                                                                   constructs
cancer
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RESULT 8
AAT59450
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AAT59432
ID AAT5
    SAXAXE
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Best Local S
Matches 20
                        31-MAY-1997
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                                                            AAT59450;
                                                                                                 AAT59450 standard;
                                                                                                                                                                                                                                                                                                                                                       Sequence 1398 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 26-28; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papilloma virus early open reading frame polyprotein constructs useful for treating, e.g. genital warts and cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cox JC, Edwards SJ, Moloney MBH, Webb EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV;
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                                                                                                                                                                                                                                                                                                                                                                                           treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-145619/13.
P-PSDB; AAW01810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1996;
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                           genital warts and cervical cancer.
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V QUEENSLAND
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                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-AU00473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                   429 A; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                 DNA;
                    entry)
                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6b E6/E7/E5a/E4 DNA cassette CSL673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frazer I,
Williams
                                                                                                 4770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wart;
                                                                                                                                                                                                                                                                            0,
                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                          Score 20; DE
Pred. No. 0.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     C; 283
                                                                                                                                                                                                318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Margetts MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condylomata acuminata;
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                                                                                                                                                                                                                                                                                                                                                     356 T; 0
                                                                                                                                                                                                                                                                                            0.48;
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                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                              Length 1398;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                          0;
Query Match
Best Local S
Matches 20
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A DNA construct (AAT59450) in vector pTrcHisA codes for an E2/E4/E5a/E5b/E6/E7/E1 polyprotein (AAW01816) of human papillomavir 6 (HPV6), plus an N-terminal hexahistidine tag. It was obtd. by amplification of the individual early genes (see also AAT59436-49) and their cloning into pTrcHisA. The DNA construct, or the encoder polyprotein, can be used as a vaccine to generate a humoral and/or cellular immune response against HPV, esp. for treating genital
                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                               Papilloma virus early open reading frame polyprotein constructs useful for treating, e.g. genital warts and cervical cancer
                                                                                                                                                                                Cox JC,
                                                                                                                                                                                                                                                                                  W09705164-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPV; polyprotein;
cervical cancer;
                                                                                              Example 6; Page 35-40; 62pp; English
                                                                                                                                           P-PSDB;
                                                                                                                                                                      Moloney MBH, Webb
                                                                                                                                                                                                 (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                            27-JUL-1995;
                                                                                                                                                                                                                                            26-JUL-1996;
                                                                                                                                                                                                                                                                13-FEB-1997.
                                                                                                                                                     1997-145619/13.
                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         papillomavirus 6 polyprotein
                                                                                                                                            AAW01816.
                                                                                                                                                                      Edwards SJ,
ÆBH, Webb EA,
                cervical
                                                                                                                                                                                                                             95AU-0004439
                                                                                                                                                                                                                                              96WO-AU00473
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "h
115..1218
                                                                                                                                                                                                                                                                                                                     /note= "HPV-6
2815..4764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                    note= "HPV-6"
                                                                                                                                                                                                                                                                                                                                                         /note- "HPV-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'function= Tag
'note= "hexaHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                          059..2508
                                                                                                                                                                                                                                                                                                                                                                                                             note- "HPV-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                               515..2808
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                                                                                                                                                                                                                                                                                                                                                                                                                                558..1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                          225..1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                 cancer
                                                                                                                                                                       Frazer I,
Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hexaHis-HPV6 polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wart;
                                                                                                                                                                                                                                                                                                                                                                                   E5b"
                                                                                                                                                                                                                                                                                                                                                                                                             E5a"
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                                                                                                                                                                                                                                                                                                                              E7 "
                                                                                                                                                                                                                                                                                                                                                        E6"
                                                                                                                                                                                                                                                                                                                                                                                                                                        E4 "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for
leader s
                                                                                                                                                                       MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       condylomata acuminata;
                                                                                                                                                                              Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                MB,
                                                                                                                                                                                McMillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purification
                                                            human papillomavirus It was obtd. by
                                 or the encoded humoral and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pTrcHisA"
                                                                                                                                                                                NAJ;
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Sequence

4770

B₽;

1597 A; 890

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1071 G;

1212 T;

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other;

Similarity 20; Conser

100.0%; llarity 100.0%; Conservative C

0;

Score 20; DB 1: Pred. No. 0.55; Mismatches

18; 0

Length 4770;

Indels

0,

Gaps

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TGCTAATTCGGTGCTACCTG

20

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RESULT 9
AAT113413
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AAT13413
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AAT13413
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AAT13413
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AAT1
AXC
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                     A DNA molecule (AAT13413) codes for human papillomavirus 6a (H the predominant HPV subtype found in biopsies of condyloma acu (benign lesions of the respiratory and genital mucosa). It was isolated from DNA extracted from a vulva condyloma acuminatum
                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                     DNA encoding human papillomavirus 6a vaccines against human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9609375-A1
                                                                                                                                  Claim 1; Fig 1A-G; 46pp;
                                                                                                                                                                                                                                                                                                                         Hofmann
                                                                                                                                                                                                                                                                                                                                                                  (MERI ) MERCK
                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 6a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT13413 standard;
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                                                                                                                                                                                                                                                                            1996-188437/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTAATTCGGTGCTACCTG
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                                                                                                                                                                                                                                                                                                                       Jansen
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                                                                                                                                                                                                                                                                                                                                                                  & CO INC
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/label- ORF-L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= major capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= ORF-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           888..4163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240..3585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695..3830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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label= ORF-E6
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16..2782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abel- ORF-E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abel- ORF-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8010
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probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunisation; condyloma acuminata;
(see AAT13414)
                                                                                                                                                                                                     6a disease, e.g. condyloma

    used to treat and in

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
complementary to
                                             It was
                                                                                       6a (HPV6a),
                                                                acuminata
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                                                 The invention relates to a method for detecting the presence of a human CC papillomavirus (HPV) subtype in a nucleic acid containing sample. The method comprises amplifying the nucleic acid in the presence of a CC method comprises amplifying the nucleic acid in the presence of a CC polymerase and a plurality of oligonucleotide sets, allowing digestion of each fluorescent probe during amplification to dissociate the fluorophore from the quencher molecule, detecting a change of fluorescence upon CC dissociation, and determining if the sample is positive for the HPV subtype if a change of fluorescence is detected in at least two emission maxima. Each oligonucleotide set mentioned above consists of an HPV discriminatory PCR primer hybridising to a first location of an HPV subtype, a reverse discriminatory PCR primer hybridising to a second clocation of the HPV subtype downstream of the first location, and a country part of the HPV subtype downstream of the first location, and a country part of the HPV subtype between the first and the second locations, where each oligonucleotide set specifically hybridises to a different HPV amplication derived from the same HPV subtype. The change of fluorescence corresponds to the occurrence of nucleic acid amplification. The method of the present invention is useful in PCR-based assays for detecting HPV subtypes in clinical samples. This sequence represents a PCR primer used to the function of the primer used in the second courter of the presents a PCR primer used in the process of the presents a PCR primer used to the courter of the presents a PCR primer used to the courter of the presents a PCR primer used to the present and the second primer used the process of the presents a PCR primer used to the present and primer used the process of the presents and primer used the process of the primer used the process of the presents and primer used the presents and primer used the process of the primer used the presents and primer used the primer used the process of the primer used the
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ABX12328/c
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Best Local S
Matches 20
                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting the presence of a human papillomavirus subtype, using multiple fluorophores, in a nucleic acid-containing sample, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-312914/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX12328 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end of the HPV subtype 6b L1 gene. The DNA can be used to devaccines against HPV6a, to treat conditions caused by HPV6a, HPV serotyping, and to produce recombinant HPV6a polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001; 2001US-314383P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002; 2002WO-US26964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fluorescent multiplex HPV PCR assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX12328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papillomavirus;
ss; polymerase;
                                     fluorescent multiplex HPV PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ζŒ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGCTAATTCGGTGCTACCTG
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20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taddeo FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2470 A; 1529 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fluorophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV;
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Pred. No. 0.58;
0; Mismatches
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                                 assay of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subtypes
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RESULT 11

RAS29985

ID AAS29985

XX AAS29985

XX AAS25

XX AAS25

XX CARS

AX CARS

AX CARS

CHICAL

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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                      18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatuc; antiprolliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperprolliferative disorder; bacterial infection; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
                                                                                                                                                                                          14-JUL-
26-JUL-
26-JUL-
14-AUG-
14-AUG-
14-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-
17-MAR-
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18; Conserv
   -2000
-2000
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2000US-0214886.
2000US-0215135.
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                                                                                                                                                         2000US-0215135

2000US-0216647

2000US-0216880

2000US-0217487

2000US-0217496

2000US-0218290

2000US-0218290

2000US-0220964

2000US-0220964

2000US-0225213

2000US-0225213

2000US-0225214
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3-0189874.
3-0190076.
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3-0184664
3-0186350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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   NOV-2000;
NOV-2000;
NOV-2000;
NOV-2000;
NOV-2000;
NOV-2000;
NOV-2000;
NOV-2000;
2000US-0241787.
2000US-0241808.
2000US-0241809.
2000US-0244817.
2000US-0246474.
2000US-0246475.
2000US-0246478.
2000US-0246478.
2000US-0246678.
2000US-0246523.
2000US-0246524.
2000US-0246525.
2000US-0246527.
2000US-0246528.
2000US-0246527.
2000US-0246527.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246527.
2000US-0246538.
2000US-0246538.
2000US-0246538.
2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246613.
2000US-0246611.
2000US-0246611.
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2000US-023365.

2000US-0234273.

2000US-0234274.

2000US-0234997.

2000US-0234998.

2000US-0235836.

2000US-0235836.

2000US-0235836.

2000US-0235836.
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2000US-0239937
2000US-0239937
2000US-0240960
2000US-0241785
2000US-0241785
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Sequences AAS2991-AAS30164 represent genomic DNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, cc mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A cc pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable cd disorders include autoimmune diseases such as rheumatoid arthritis, chyperproliferative disorders such as neoplasms of the breast or liver, cc disorders such as cerebral ischaemia, nervous system disorders such as cardiac arrest, cerebrovascular cd disorders such as corneal infection, endocrine disorders such as corneal infect
                                                        Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-457723/49
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                                                          l Similarity
17; Conser
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                      TGCTAATTCGGTGCTACCT
   Barash SC,
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2000US-0251989.
2000US-0251990.
2000US-0254097.
2000US-0259678.
                                                          Conservative
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2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0249299.
2000US-0249300.
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2000US-0251030.
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2000US-0249264.
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2000US-0249213.
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2000US-0249216.
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2000US-0249210
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                                                                         79.0%;
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                      19
                                                                         Score 15.8;
Pred. No. 8
                                                          Mismatches
                                                                         No. 80;
                                                                                            DВ
                                                                                          22;
                                                      2;
                                             Indels
                                                                                        Length
                                                                                            281;
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   RESULT 12
AAS28494
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14-AUG-2000

14-AUG-2000

14-AUG-2000

11-AUG-2000

11-AUG-2000

22-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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02-MAR-2000;
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17-MAR-2000;
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                  2000US-0229344.

2000US-0229345.

2000US-0229509.

2000US-0229513.

2000US-0230437.

2000US-0230438.

2000US-0231242.

2000US-0231242.
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2000US-0227009.

2000US-0228924.

2000US-0229287.

2000US-0229343.

2000US-0229344.
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2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-0186350
2000US-0189874
2000US-0190076
2000US-0198123
2000US-0205515
2000US-0209467
                                                                                                                                                                                                                                                                       2000US - 0225268
2000US - 0225270
2000US - 0225447
2000US - 0225475
2000US - 0225758
2000US - 0225758
2000US - 02256279
2000US - 0226681
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2000US-0220964.
2000US-0224518.
2000US-0224519.
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(HUMA -)

WPI; Rosen

Claim 1;

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12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000;

26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000;

21-SEP-2000; 25-SEP-2000; 25-SEP-2000;

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RESULT 13
AAS29864
ID AAS298
XX AS29
XX AS29
XX 21-NC
DT 21-NC
DT 21-NC
XX Lung
KW Lung
KW Chick
KW antir
KW antir
KW antir
KW apter
KW Opher
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AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printe seguince of the value of the printe securics of the value of the printe seguince of the printe seguince of the value of the printe seguince of the value of the printe seguince of th
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             Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss; hyperproliferative disorder; breast; liver; cardiovascular disorder; ss;
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  bacterial infection;
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2000US-0249216
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21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CCT-2000; 20-CC
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RESULT 14
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11-DEC-2000;
05-JAN-2001;
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                                                                                                                                                        Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAS29839-AAS29930 represent cDNA molecules, which encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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  31-JAN-2000; 2000US-0179065
                             17-JAN-2001; 2001WO-US01333
                                                                                     WO200155448-A1
                                                                                                                                                                                                                Novel cDNA encoding
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DB; AAU18577.
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; 2000US-0254097.
; 2001US-0259678.
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    Isolated polypeptide disorders related to cancers and also for
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RESULT 15
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                                                                                                         Detection of expression the fermentation and gro
                                                                                                                                                                                                  (NAAD-)
(NARE-)
(NORQ)
                                                                           Claim 1;
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                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag;
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                                                                                                                                                                 Kobayashi
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89.5%;
                                                                                                         ion of specific Aspergillus genes growth conditions of the fungus,
                                                                                                                                                                 Kashiwagi Y,
i T, Kitamoto
                                                                                                                                                                                                                                                                                                                                                           gene; ss.
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                                                                           Sequence Listing;
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N, Gomi
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Abe K;
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising

polynucleotides

for monitoring

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progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for funguary for functions of the printed Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                   Sequence 907 BP; 249 A; 208 C; 205 G; 243 T; 2 other;
Length 907;
                                                                                                               Indels
                                                                                                            0;
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3333333¥& γ Search completed: August 23, 2003, 10:38:19 Job time: 208.5 secs 밁 Query Match 79.0%; Score 15.8; DB 25; Best Local Similarity 89.5%; Pred. No. 91; Matches 17; Conservative 0; Mismatches 2;

ли́д 25 09:29:25 2003

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Title:
Perfect score:
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Listing first 45 summaries
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Pred. No.

is

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 23, 2003, 08:28:23; Search time 993 Seconds (without alignments) 823.960 Million cell updates/sec

Run on:

RESULT 1 AX301234 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISI REFERENCE AUTHORS TITLE JOUKNAL	1 18 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0000	Result No.
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linear I	AF4781521 AF4781521 AF478153 AF478155 AF478155 AF478155 AF478159 AF478159 AF478160 AF478161 AF478161 AF478163 AF478163 AF478166 AF47	220000000000000000000000000000000000000	Description AX301234 Se
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RESULT 3
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S JP 1993192200-A/27.

Synthetic construct
Synthetic construct
artificial sequences
1 (bases 1 to 20)
HORS Okazawa, K., Shimada, M., Katou, I., Fukushima, M. and Fujinaga, K.
DETECTION OF HUMAN PAPILLOMA VIRUS
Patent: JP 1993192200-A 27 03-AUG-1993;
                                                                                                                                                                                                                                           Local
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TAKARA SHUZO CO LTD
OS Artificial gene
OC Artificial seque
PN JP 1993192200-A/
PD 03-AUG-1991 JP 1
PR 20-AUG-1990 JP 9
PI OKAZAWA KAZUHIDE
FUXUSHIWA MICHIO,
PI FUJINAGA KEI
PC C12Q1/70,012Q1/6
CC Strandedness: Si
CC topology: Linear
CC hypothetical: No.
CC anti-sense: No.
                                     synthetic construct
                                                E05247.1 GI:2173437
JP 1993192200-A/17.
                                                                                 Part of DNA sequence E05247
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                       Primer for amplifying Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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C12Q1/70,C12Q1/68;
strandedness: Single;
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20-AUG-1990 JP 90P 217067
OKAZAWA KAZUHIDE, SHIMADA M
                                                                                                                                                                                                                                                                                                                                                                                             hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OS Artificial gene
OC Artificial gene
OC Artificial sequence; Genes.
OS Human papillomavirus
PN JP 1993192200-A/17
PD 03-AUG-1993
PF 19-AUG-1993 JP 1991230839
PR 20-AUG-1990 JP 90P 217067
PI OKAZAWA KAZUHIDE, SHIMADA MASJ
FUKUSHIMA MICHIO,
PI FUJINAGA KEI
PC C1201/70,C1201/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
                                                                                                                                                                                      Submitted (26-FEB-1992) Kei Fujinaga, Cancer Research Institute, Sapporo Medical College, Department of Molecular Biology; S1, W17 Chuo-ku, Sapporo 060, Japan (Tel:011-611-2111, Fax:011-615-3099) Location/Qualifiers
                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                               2 (bases 1 to 803) Fujinaga, K.
                                                                                                                                                                                                                                                                                           Fujinaga,K.
Unpublished
                                                                                                                                                                                                                                                                                                              Papillomavirus.
1 (bases 1 to 803)
                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus
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D10597.1 GI:535788
                                                                                                                                                                                                                                                                                                                                                                                       E6 protein;
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1 (bases 1 to 20)

Okazawa,K., Shimada,M., Katou,I., Fukushima,M. and Fujinaga,K.

DETECTION OF HUMAN PAPILLOMA VIRUS

Patent: JP 1993192200-A 17 03-AUG-1993;

TAKARA SHIZO CO LTD

OS ARTIGICA, ON TO THE PARKARA SHIZO CO LTD
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CITCQKPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
                                                                                                                     /organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="Type Sapporo-A"
/db_xref="taxon:10566"
                                                                                           codon_start=1
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/db_xref="taxon:32630"
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VERSION
KEYWORDS
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PPH35CG
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Best Local S
Matches 19
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MEDLINE
PUBMED
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                                           gene
      Sg
                                                                                                                                                                                                                                                     CAAT_signal protein_bind
                                                                                                                                                                                                                                                                                                                    protein_bind
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||||||||||||| ||||||||
367 TGTCAAAAACCGCTGTGTCC 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 7851)
Marich,J.E., Pontsler,A.V., Rice,S.M., McGraw,K.A.
Dubensky,T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome; major capsid protein; minor capsid protein; regulatory protein; regulatory protein; replication protein; transformer protein Human papillomavirus type 35

Human papillomavirus type 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type M74117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Human papillomavirus type 35 carcinoma DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human papillomavirus type
Virology 186 (2), 770-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The phylogenetic relationship and complete nucleotide sequence human papillomavirus type 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 159, 187-190 (1991)
87265470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lorincz,A.T., Quinn,A.P., Lancaster,W.D. and Temple,G.F.
A New Type of Papillomavirus Associated with Cancer of the Uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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127 c 190 g 204 t
                                                                                      /function="gene transcription"
54. .59
                                                                                                                                                                                                                                                                         complement(18. .26)
                                           /note-"putative"
110. .559
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110. .559
                                                                                                                                                                                                                             note-"putative"
                                                                                                                                                                                                                                                                                                                                            /standard_name="LCR"
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/oin(7092. .7851,1. .109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                               'note-"putative"
                                                                                                                                                                                        function="gene transcription"
                                                                                                                                                                                                              bound_moiety="E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism-"Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                   function="regulatory region"
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95.0%;
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Pred. No. 41;
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pe 35
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/note="putative"
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/codon_start=]
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NTTPFTHTKACSVGTTETQKTHKKLRGGTELFYNPTKKVRLSAVDSVDRGYYSTSDCT
NTTPFTHTKACSVGTTETQKTHKKLRGGTELFYNPTKKVRLSAVDSVDRGYYSTSDCT
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EDMYDFINDTDILNIQAETETAQALFHAQEEGTHKEAVQVLKRKSSFLSSVSLCVN
NNISPRIKAJCIENKNYAAKRALFELPDSGYGNSEVEHHEIQOVEGHDYVEQCSMSGE
DSITSSSDERHDETPTRDIIQILKCSNANAAMLAKFKELFGISFTELIRPFKSDKSTC
TDWCVAAFGIAPSVANFKHITYVYIYNVYRVHCAMVILALLFKYEKREQOLKTIDAK
LLCISAASMLIQPFKLRSTPAALVFKTYAMSHISEVDGETPENIQRGYTVLOHSFNDI
FDLSEMVQWAYDNDFIDDSDIAYKYAQLAETNSNACAFLKSNSQAKIVKDCATMCRHY
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NCILIYGAPNTGKSLFGMSLMHFLQGAIISYVNSKSHFWLQPLYDAKIAMLDDATSPC
GIYRPIFKKCTRWKSYISFRCKALSIVHIMPTFTYYININAGKDDRWPYLHSRVVVFT
/product="unknown"
/protein_id="AAA46965.2"
/db_xref="GI:20522255"
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868. .2760
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QakpDtsnynivtscckceatlrlcvQsthiDirkledllmgtfgivCpgcsqra"
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405..416
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                                                                                                                                                                                                              NKDRCGSCSTTTPIVHLKGDANTLKCSRYRLGKYKALYQDASSTWRWTCTNDKKQIAI
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/gene="E2"
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/gene="E2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="replication protein"
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/gene="E7"
                                                                                                                                                                                          /TLTYTTEYQRDKFLTTVKIPNTVTVSKGYMSI "
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/protein_id="AAA46966.1"
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                                                                                                        'gene="E4"
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/note="putative; E6 ORF from bp
                                                                                    'note="putative"
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repeat_region repeat_region protein_bind
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3793. .4039
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TFTDPSVLHPPTPAETSGHFVLSSSSISTHNYEEIPMDTFIVSTDSNNITNSTPIPGS
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TGVEVGGGDFJOGGGTPCNANQVKAGECPPLELLNTVLQDGDMYDTGFGAMDFTTLQA
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ELQPLQHPSSLEHTTVSTSLANGMFDIYAPIDTEEDIIFSASSNNTLYTTSNTAYVP
SNTTIPLSSGYDIPTIAGAPDIVFNSNTITNSVLPVPTGPIYSIIADGGDFYLHPSYYL
LKRRRKAIPYFFADVSVAV"
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VLIIMVTVATPILIAFVVSCFCIYIMMINAHAQYIAVQ"
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7671. .7676
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(CK-octomer)"
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complement(7670...76
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/bound_moiety="hormone receptor"
7514. .7519
                                                                                                                                                                                                                                                                                                             /function="gene transcription" 7477. .7491
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VDTTRSTNMSVCSAVSSSDSTYKNDNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYI
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/codon_start-1
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/gene="E5"
                                                                                                                                                               /bound_moiety="NF-1"
7534. .7539
                                                                                                                                                                                                                        /bound_moiety="NF-1"
                                                                                                                                                                                                                                                                                                                                                                  /note="putative"
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                                                                                                                                                                                                                                                                                                                                                   /bound_moiety="E2"
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                                                                                                                        .7677)
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ORGANISM
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AUTHORS
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ACCESSION VERSION
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HPV35H
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TITLE
JOURNAL
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JOURNAL
MEDLINE
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X74477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 35H
Human papillomavirus type 35H
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGTCAAAAACCGTTGTGTCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delius.H.
Direct Submission
Direct Submission
Submitted (06-AUG-1993) H. Delius, Deutsches
Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 El gene; E2 gene; E4 gene; I
gene; L2 gene; late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delius, H. and Hofmann, B.

Primer-directed sequencing of human
Primer Top. Microbiol. Immunol. 186,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Papillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 7879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heidelberg, FRG
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                                                                                                                                                                                                                                                                                                           562. .861
/gene="E7"
                                                                                                                                                                                                                                                                                                                                                                                     /product="early protein"
/protein_id="caa52561.1"
/db_xref="G1:396998"
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FACYDLCIVYREGQPYGVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIR
CITCQXPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E2 gene; E4 gene; E6 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety="NF-1"
1343 c 1568 g
                                                                                                                                                               /translation="mHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEEDTIDGPAG
QAKPDTSNYNIVTSCCKCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQRA"
                                                                                                                                                                                                                                                                                                                                                                        562. .861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110.
                                                                                                                                                                                                                          /product="early protein"
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/db_xref="GI:396999"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Human papillomavirus type 35H"
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/db_xref="taxon:31551"
/codon_start=1
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/db_xref="GI:397000"
                                                                                                                      'gene="El"
                                                                                                                                                                                                         /db_xref="SWISS-PROT:P27230"
                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                 /gene="E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="E6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="E6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="insert in BamHI site of pBR322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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95.0%;
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Pred. No. 43
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13-31 (1994)
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RESULT 7
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Best Local :
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                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                          /gene="L1"
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TGVEVGRQCPLGVGISGHPLLNKLDDTENSNKYGNGSTDRECISMDYKQTQLCLIG
GREPTGEHWGKGTPCNANQVKAGECPPLELLNTVLQDDDMVDTGFGAMDFTTLQANKS
DVPLDICSSICKYPDYLKMVSEPYGDMLFFYLRREQMFVHLFNRAGTVGETVPADLY
IKGTTGTLPSTSYFPTPSGSMVTSDAQIFNKFYWLQRAQGHNNGJCWSNOLFVTVVDT
TRSTNNSVCSAVSSDSTYKNDNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYTHSM
NPSILEDWNFGITPPPSGTLEDTYRYVTSQAVTCQKPSAFKFKDDPLKNYTFWEVDLK
NPSILEDWNFGITPPSGTLEDTYRYVTSQAVTCQKPSAFKFKDDPLKNYTFWEVDLK
EKFSADLDQFPLGRKFLQAGLKARPWERLGKRAAPASTSKKSSTKRRKVKS"
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2714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRHKRSTKRVKASATQLYRTCKAAGTCPDDVIPKVEGNTVADQ
ILKYGGMAVEFGGLGIGSGSGFGGRSGVPLCTTPPTAATNLE RPVTVESIPLDTI
GPLDSSIVLVEETSFIESGAPVVTPRVPDTTGFTITTSTDTTPAILDVTSISYHDND
TETDBYLHPPTPAETSGHFVLSSSISTHNYEBIPKDTFIVSTBUNGS
RPTTRLGLYSKGTQQVKVVDPAFMTSPAKLITYDNPAYEGLNPDTTLQFEHEDISLAP
DDEFMDIIALHRPALTSRKGTIRYSRVGNKRTMHTRSGKAIGARVHYYQDLSSITEDI
ELOPLOHVPSSLPHTTVSTSLNDGMFDIYAPIDTEDIIFSASSNVTLYTTSNTAYVP
SNTTIPLSSGYDIPITAGPDIVNNNTITNTVLPVPTGPIYSIIADGGDFYLHPSYYL
LKRRRKRIPYFFADVSVAV"
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UNNISPRLKAICIENKNTAAKRRLFELPDSGYGNSEVETQQIQQVEGHDTVEQCSMGS

GDSITSSSDERHDETPTRDIQILKCSNANAMLAKFKEISTELLFERKSKST

CTDMCVAAFGIAPSVARSLKTLIKPYCLYIHIQCLSCSWGMVILALLREKCAKNRTI

EKLLSKLLCISAASMLIQPPKLRSTPAALYWFKTAMSNISEVDGETPEWIQRQTVLQH

SFNDAIFDLSEMVQWAYDNDFIDDSDIAYKYAQLAETNSNACAFLKSNSQAKIYKDCA
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HGVPKKNCILIYGAPNYGKSLFGMSLMHFLQGALISYVNSKSHFUAQFLYDAKIAMLD
DATSPCWAYIDQYLRUALDGNPISLDVKHKALVQLKCPPLLIYSNINAGKDDRMPYL
SRVVVFTFHNEFPFDKNGNPVYGLNDKNWKSFFSRTWCRLNLHEEEDKENDGDAFPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="L1"
5601. .7109
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4211. .5620
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/db_xref="GI:584036"
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/gene="E2"
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                                                                                                                                                                                                                                                                                                                                               1339
                                                                                                                                                                                                                                     92.0%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 31
Human papillomavirus type 31
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted
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1 (bases 1 to 7912)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nal source text: Human papillomavirus type 31 DNA. entry and computer-readable copy of sequence [1] kindly tted by M.D. Goldsborough, 05-JUL-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ORF E7 from bp 545 to 856"
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                                                                                                          /codon_start=1
                                                                                                                              note="ORF L1 from bp 5516 to
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423 TGTCAAAGACCGTTGTGTCC 442
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Deng,W., Burland,V., Plunkett,G. III, Boutin,A.,
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S.,
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Pla
Straley,S.C., McDonough,K.A., Nilles,M.L., Matson
Batther,F.R. and Perry,R.D.
Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
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19; Conser
                                                                                                                      Submitted (21-FEB-2002) Genetics, University Henry Mall, Madison, WI 53706, USA Location/Qualifiers
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Yersinia pestis KIM
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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GCKPPIGEHWGKGSPCSNNAITPGDCPPLELKNSVIQDGDMVDTGFGAMDFTALQDTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="keratinocyte-dependant enhancer" 7868. .7879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDTTRSTNMSVCAAIANSDTTFKSSNFKEYLRHGEEFDLQFIFQLCKITLSADIMTYI
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7406. .7420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name="glucocorticoid responsive element"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative"
7291. .7302
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1364 c 1572 g 2448 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="gene transcription'
542. .7549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bound_moiety="E2"
                                                                                                       .10909
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95.0%;
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of 415 of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R., Plana,G.V., Matson,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                           of Wisconsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwartz, D.C.,
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/gene="usg" /note="synonym: y1598"

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/codon_start-1
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2901. .3971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"dedA"
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2137. .2826
/gene-"dedA
/gene-"dedA
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to residues 1 to 216 of 219 from E. coli K12: B2317;
residues 1 to 215 of 229 are 85.18 pct identical to
residues 1 to 216 of 219 from GenPept : >gb|AAL/21268.1|
(AE008806) putative DedA family [Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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MPLDAEKMERAAQCLLGENDFTSFRAVQCQSRTPWRNVKHVKVTRHGAYIVVDIKANA
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/function="enzyme; aminoacyl tRNA synthetases, tRNA
modification"
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/note="synonym: y1599"
1126. .2007
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LY"
1126. 2007
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VRKVLODEGLPITVSCIQSPVFYGHAQVVHLEALRPIAAEEARSELENCDDIQLSEED
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                                                                                                                                            /gene="accD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative"
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VGQAYVVQLGALKNAAKVNEIVAMLRLSGHRAFTVPATTPVQGEITRLYVGPDASKQKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="dedD"
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/function="putative membrane"
/function="putative membrane"
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-ygb|AAG57443.1|AE005463_6 (AE005463) putative lipoprotein [Escherichia coli 0157:H7 EDL933]"
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ALIGFAGPRVLEQTVEEKLPGGFQRSEFLIEKGAIDMIVRRFVMRQTLASILSKLTHQ
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4142. .5524
/gene-"folC'
/function-"enzyme; biosynthesis of cofactors, carriers:
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//note-"residues 53 to 350 of 356 are 86.24 pct identical //note-"residues 1 to 296 of 304 from E. coli Kl2 : B2316; to residues 1 to 296 of 356 are 86.91 pct identical to residues 53 to 350 of 356 are 86.91 pct identical to residues 1 to 296 of 304 from GenPept : >gb|AAL21267.1| (AE008806) acetylCOA carboxylase, beta subunit [Salmonella typhlmurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11/
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5638. .6366
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component, beta subunit"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start-1
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RESULT 9
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LOCUS
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                           Agrobiological Sciences, Rice Genome Research Program; Kannondai Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Oct 26, 2002 this sequence version replaced gi:22775423.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN,html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://www.softberry.com/), GeneMark.hmm
(http://www.tigr.org/tdb/glinmerm/glmr.form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://foinformatics.lastate.edu/Ggi-lin/sp.cgi), BLASTN and
BLASTX. The genomic sequence was searched against NCBI NonRedundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering
                                                                                                              (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDHJ accession no. and RGP clone ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in Database (2001)
2 (bases 1 to 102178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone:0J1060_D03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP003803.3 GI:24414010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC clone:OJ1060_D03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP003803
                                                                                                                                                                                                                                                         Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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//gence"cvpA"
/function="membrane; colicin'related functions"
/note="required for colicin V production; residues 1 to
160 of 169 are 83.12 pct identical to residues 1 to 160 of
162 from E. coli Kl2: B2313; residues 1 to 160 of 169 are
83.12 pct identical to residues 1 to 160 of 167 from
GenPept: '9b|ARL21264.1| (AE008806) membrane protein
required for colicin V production [Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"membrane protein"
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/protein id-"AAN85173.1"
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/translation-"MYMBYVIIGIIGFSALVSLIRGFVREALSLVTWGCAFFVASHF
/TYLAVYFTRFEDEIVRNGIAIGILFIATLIVGAIVNYVISSLVERTGLSGTDRVLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: y1604" 6663. .7172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLN 26-OCT-2002 chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7,
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     CDS
                                                          gene
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                                                                                                                                                                                                                                                                                                                                        JOHN (**--
11030. 11337)
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/oin(8621. _8754,8874. .8983,9860. .9930,10812. .10932,
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IVAGASGSAHFPYMPTGDNVLNTPAWGLHITPRAPEOCHTQHTYDEYGSASTHHGVPA
YSPRTAFIEDFFSTDPPQEEYGMDYWHAAPQVTQPTQETEAGQGPDVTPQQTARDRHP
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/db_xref="GI:24414012"
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/translation="MERRLTPGYSLSSSLSSLSLFFAGSAGTDGLVGSGAAAGDLGEAAP
VVGEDEMLHTISLTPFVIPLPSLSSSLSSLSLFFAGSAGTDGLVGSGAAAGDLGEAAP
SSPPSLSGDGLHAAPGPVASNDNDDMVGSCNCLWLKRHPLVCGSIIVINPVTGESLHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein predicted by GeneMark.hmm etc./codon_start=1
     12019. .12453
/gene="OJ1060_D03.5"
12019. .12453
                                                                                       PDNLTYPTEQIRRRKKGGPSKRAKGTDRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(8621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPPLATSRSRHAGMISFGYHSTTGKYKIVHFPSNGGLVDEVTLGGTASSSSPPAMAA
                                                                                                                                                                                                                                                                                   /note="mutator-like transposase-like
/codon_start=1
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8754,8874. .8983,9860. .9930,10812. .10932,

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'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OJ1060_D03 clone has an overlap with OJ1127_E01 clone(DDBJ: AP003747)at 5' end and an overlap with OJ1113_E01(DDBJ: AP005437) at 3' end. The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         almost the entire length of partial sequence) is classified as an
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This category is n hypothetical ORF predicted by GlimmerM" complement(4270. .4578) /gene="0J1060_D03.2" complement(4270. .4578)
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1311. .1511
complement(join(5870..6466,6570.
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complement(join(5870..6466,6570../gene="OJ1060_D03.3"
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HPSILATCDDGLGPFLDGASPPRLLLFLAAGADVVVDAGRAFSAGGRVYERSAASWRS
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1311. .1511
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein
predicted by GeneMark.hmm etc."
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/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                               /gene="0J1060_D03.2"
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                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .102178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (japonica cultivar-group)"
                                                                                                          .6647))
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CDS
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/note-"probably inactive due to frameshift(s)
probably inactive due to stop codon(s) in CDS
pseudogene, hydroxyproline-rich glycoprotein"
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EATARYDGGVGAGMP"
                                                                                                                    predicted by gm etc."
/codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein predicted by GENSCAN etc."
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/gene="0J1060_D03.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MRCAMINHRLFDHARARVQSAHLLTVNTVPSPLLAALPNVRRCH LPNGEKKTPPKRSRCLHVSTSHRAKAATPMPITPYXSSGGSNARGRGPSRSGARAAA AATWHGEEQTNGKKGDSLLPQPPKVKPPGAMCWPPAHAMAP"

Join (12948 . 1428, 15290 . .15376, 16109 . .16198)
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36755. .37150
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="0J1060_D03.10"
28336. .31791
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/gene="OJ1060_D03.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(19591. .19658,20059. .20179))
/gene="OJ1060_D03.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(19591. .19658,20059.
/gene="OJ1060_D03.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVVPLIHLVGERGSGTSEKAMVVLASLAGIVEGRDAVVEAGGIPALVETIEDGPARE
REFAVVALLQLCSECPRNRALLVREGAIPPLVALSQSGSARAKHKAETLLGYLREQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="avslagsqipspgqspcaaarsqrrgagysmrtirsallqpdsc
pgsphyaaaydaagadsdmemutdsvidphlselaatagapahpayaksssanaaate
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aaplervepfylacyralgpdaapdarrtaaarirllakhrsdireligysgaipalv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pseudogene, Taml transposon protein TNP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted by GENSCAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGCRVEPVAASSLAFIVLRCVTFSLTPTSGSAAPSIWVTYSYT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLRSTDPVAQESAVTALLNLSLEERNRSAITAAGAIKPLVYALRTGTASAKQNAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted by GlimmerM etc."
                                                                                                                                                                                                      /gene="0J1060_D03.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="deletion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"OJ1060_D03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSLSGIEENRATIGACGAIPPLVALLSAGSTRGKKDALTTLYRLCSARRNKERAVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAC22265.1"
/db_xref="GI:24414015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="arm repeat containing protein homolog-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(12948. .14258,15290. .15376,16109.
/gene="OJ1060_D03.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAC22264.1"
/db_xref="GI:24414014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xref="GI:24414014"
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                                                                                                                                                                                                                                                                                                                                                                                                    in CDS
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SOURCE
ORGANISM
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AC107604/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Blswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Haves, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hulgk, S., Hume, J., Idlabird, D., Jackson, A.,
Jacob, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
                                                                                                                    Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Maheshwari, M., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Meenen, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, S., Munidasa, M., Nurphy, M., Nair, L., Naris, S., Munidasa, M., Nurphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nunjah, M., Norris, S., Nankervis, C., Neal, D., Newton, N., Norris, S., Nurphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Oliroz, J., Rachin, E., Reeves, K., Regler, M.A., Reigh, R., Paster, M., Parks, K., Paster, M., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84821
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Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rivės,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
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Rattus norvegicus clone CH230-196K4, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC107604.4 GI:23266137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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AU183957(R0167),D46798(S11701),AU077610(E20630)
Similar to Arabidopsis thaliana chromosome5, At5g55530
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="OJ1060_D03.12"
38163. .39500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38163. .39500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPEASRWMPLLDFFGPYRSKPWKKNGSKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAC22268.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="0J1060_D03.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 102178,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams, C., Alder, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                   misc_feature
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Direct Submission
Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 223885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21737824.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                     the accession number will be preserved.

1 223885: contig of 223885 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                              by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program. Phrap; version 0.990329
Consensus quality: 212075 bases at least Q40
Consensus quality: 215656 bases at least Q30
Consensus quality: 214464 bases at least Q30
Estimated insert size: 222767; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GPUL Center clone name: CH230-196K4 Center clone Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
.----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
                                          1866.
                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                           /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                    /clone="CH230-196K4"
note="clone_boundary"
                                                                                                                                                                                                           /db_xref="taxon:10116"
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                                          . 2449
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                                  Bryant, N., Bladri, J., Blankenburty, N., Bryant, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Cadleron, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Ding, Y., Dinh, H., Divya, K., Davalla, M.L., Davalla, M., Durbin, K., Duvall, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Franser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, J., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Hernandez, J., Havlak, P., Haves, A., Henderson, A., Hogues, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Hully, S., Hume, J., Idlebird, D., Jackson, A., Hogues, M., Kelly, S., Kelly, S., Khan, Z., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Mahshwari, M., Mahindarthe, M., Mahmoud, M., Malloy, K., Mangum, A., Martin, R., Martinez, E., Motemayor, J., Moore, S., Milosa, E., Motemayor, J., Moore, S., Milosa, E., Montemayor, J., Moore, S., Milosa, M., Walloy, K., Martin, R., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pilmus, E., Phyl. -L., Pilmus, E., Phyl. -L., Reith, R., Regier, M. A., Reith, R., Reves, K., Regier, M. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
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Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.
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222550. .223885
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                           Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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94.7%;
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Pred. No. 1.7e+02;
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, *** SEQUENCING
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IN PROGRESS ***.
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On May 9, 2003 this sequence version replaced gi:23265564.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 236021: contig of 236021 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: CH230-4E17

Assembly program: Atlas;
Consensus quality: 218135 bases at least Q40
Consensus quality: 221412 bases at least Q20
Consensus quality: 223855 bases at least Q20
Estimated insert size: 22984; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: GAUD Center clone name: CH230-4
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                                                                                                         /mol_type="genomic
                                                                                                                                                                                    1. .23602
                                                                                                                                                                                                                  Location,
                                     /clone="CH230-4E17"
                                                                   /db_xref="taxon:10116"
                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                  /Qualifiers
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ACCESSION
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              Allyalebechi, V., Abyagi, A., Ayoleji, R., Bacca, E., Baucei, M., Baldarnaike, D., Barber, M., Barnstead, M., Beahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, C., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, G., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Carde, M., Garcia, A., Garner, T., Garza, M., Eggan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Eggan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Eggan, A., Escotto, M., Hamilton, C., Hamilton, C., Hamilton, K., Duval, B., Eaves, M., Gabregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A., Liu, Y., Lebow, H., Levan, J., Lewis, L., Kovar, C., Kovar, C., Kovar, C., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., London, P., Longacre, S., Lopez, J., Liu, J., Mahindartne, M., Mahndartne, M., Mahn
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Rattus norvegicus
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Rattus norvegicus clone CH230-11H4, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC105688.3 GI:23264260
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232901. .236021
/note="wgs_end_extension
clone_end:T7"
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complement(229315. .230090)
/note="clone_boundary
clone_end:T7
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clone_end:Sp6"
5478. .6115
/note="clone_boundary
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94.7%;
Okwuonu, G.,
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Pred. No. 1.
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Olarnpunsagoon, A.,
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On Sep 21, 2002 this sequence version replaced g1:21743898.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotunn sequence reads. Both end sequences and whole genome shotunn sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Sequencing Consortium Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
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                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                            be preserved
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                                                                                                                                                                 234225
234325
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Consensus quality: 200479 bases at least Q40
Consensus quality: 204791 bases at least Q30
Consensus quality: 207411 bases at least Q30
Consensus quality: 207411 bases at least Q30
Estimated insert size: 251580; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-11H4
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                                         /organism="Rattus norvegicus"
                                                                                      1. .236062
                                                                                                                   5 236062: contig of 1738 bp in length Location/Qualifiers
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baylor
                                                                                                                                                                                                  234224: contig of 234224 bp in length 234324: gap of unknown length
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AJ414153
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-OCT-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                       (URL,
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1 (bases 1 to 258050)
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complement(231465. .2
/note="clone_boundary
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/clone="CH230-11H4"
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                                                                                                                                                                                                 /mol_type="genomic
/strain="CO92"
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/note="no significant database hits"
/codon_start=1
                                                /gene="YP02590"
                                                                                                 /gene="YP02590"
                                                                                                                                                note="biovar:
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                                                                                                                                                                                                                        /organism="Yersinia pestis CO92"
/mol_type="genomic DNA"
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                                                                                                                                                                      /note="one of 9 probable for YPO2592 by TMHMM2.0" formplement(1569...1634)
                                                                                                                                                                                                                                                               /note="one of 9 probable for YPO2592 by TMHMM2.0" complement(1497. .1547) /gene="YPO2592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="one of 9 probable transmembrane helices for YPO2592 by TMHMM2.0" complement(1206. .1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="one of 9 probable transmembrane helices for YPO2592 by TMHMM2.0" complement(11101. .1186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="Sptrembl:@8zdh6"
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QYFRLWTWIFYYMTGRFLCSRICQKMTKLPKVRLAAKILLLPTSISMYYYESFMSIYV
YKTVNASYFLDNFHYLVLSICLFVIFDNFDTQYEWIKKTLAYISPSMIGVYILHDGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(972. .1937)
/gene="YPO2592"
complement(972. .1937)
/gene="YPO2592"
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/gene="YPO2591"
complement(608. .790)
/gene="YPO2591"
                                                                                                                                                                                                                                                                                                                                                           complement(1401. .1451)
/gene="YPO2592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1308. .1361)
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TTIEVHITQVAYLISV"
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                                                                                                    /note="one of 9 probable for YPO2592 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="one of 9 probable
for YPO2592 by TMHMM2.0"
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/db_xref="GI:15980579"
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                                                                                                                                                   /gene="YP02592"
                                                                                                                                                                                                                                                          /gene="YP0259:
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for YPO2592 by TMHMM2.0"
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                                                                                                                                                                                                                                                                                                 /note-*Similar to Escherichia coli probable cold shock protein CspE SW.CSPE ECOLI (P36997) (68 aa) fasta scores: E(): 1e-25, 94.1% id in 68 aa, and to Vibrio cholerae hypothetical protein TR:AAC73388 (EMBL:AE098260) (69 aa) fasta scores: E(): 3.1e-26, 94.2% id in 69 aa. Similar to YPO1746 (84.1% identity in 69 aa overlap), YPO1655 (83.3% identity in 66 aa overlap), YPO3644 (73.6% identity in 72 aa overlap), YPO3643 (72.2% identity in 72 aa overlap), YPO3643 (73.2% identity in 72 aa overlap), YPO3669 (63.9% identity in 72 aa, overlap) and YPO398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3297. .3668)
/gene="YPO2594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Predicted helix-turn-helix motif with score 1182 (+3.21 SD) at an 163-184, sequence FSGGDIARILKKSEKTVSGQKR" complement(3297. .3668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to Salmonella typhimurium fimbriae W protein FimW SW:FIMM_SALTY (P37928) (198 aa) fasta scope(): 0.0066, 21.9% id in 178 aa, and to C-terminus of Erwinia amylovora activator of exopolysaccharide synthesis, RCSB TR:P96320 (EMBL:Y09848) (215 aa) fasta scores: E(): 0.0003, 43.7% id in 71 aa"
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/genė="YPO2592"
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Afysadvifigvdefsffealkkldktpaeadvflicdarlnsflqgiprfsdvtmif
Redsletvsnkiayyfkrkfrgfkdbklierktakvlhlvsserqyltpnenivlklfn
Egfsggdiarilkksektvsgqkrsamkklgartdvelikmfmfk"
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/db_xref="GI:15980580"
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for YPO2592 by TMHMM2.0"
2360. .2977
                                                                       AEGORVEFEITNGAKGPSAANVIAI"
                                                                                                                                                /product="putative cold shock
/protein_id="CAC92838.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIKKGAEVTFEPTTNTKGLSAFAVKVAIESKYIFIANERIKLTS
IKSFNTFTKEVPAQAEVDKANTILSVNLLMNKIRPQEEDISEKTIPLKMLSITTFQNV
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                                                                                                                                                                                                                                                                               (53.6% identity in 69 aa
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/gene="YPO2593"
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RESULT 15
AF234529
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AUTHORS
TITLE
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Best Local
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OC Artificial ge
OC Human papillo
PN JP 193192200
PN JP 193192200
PN JP 19319290
PF 19-AUG-1991 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PR 20-AUG-1990 J
PR 70-AUG-1990 J
PR 70-AUG-1990 J
PI FUJINAGA KEI
PU C12Q1/70,C12Q
CC strandedness:
CC toppology: Lin
CC hypothetical:
CC anti-sense: N
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1 (bases 1 to 20)

Okasawa,K., Shimada,M., Katou,I., Fukushima,M.

DETECTION OF HUMAN PAPILLOMA VIRUS

Patent: JP 1993192200-A 21 03-AUG-1993;

TAKARA SHUZO CO LTD

TAKARA SHUZO CO LTD
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 AF234529
AF234529.1
                                       Human papillomavirus type
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                                                         AF234529
                                                                                                                                         TGTCAAAAACCGTTGTGTCC
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Artificial sequence; Genes.
Human papillomavirus
JP 1993192200-A/21
03-AUG-1993
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C12Q1/70,C12Q1/68;
strandedness: Single;
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20-AUG-1990 JP 90P 217067
OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of DNA sequence of
                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                     topology: Linear; hypothetical: No;
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/note="synonym: YPO2596"
complement(4686. .5069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00352 'Cold-shock' DNA-binding domain signature." complement(4686. .5069)
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                                                                                                                                                                                                                                                     /organism-"synthetic construct"
/mol_type-"genomic DNA"
/db_xref="taxon:32630" 7 t
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GI:7331167
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94.7%;
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90.0%;
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Pred. No. 3.1e+02;
0; Mismatches 2;
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protein gene, complete
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE
AUTHORS
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AUTHORS
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Search completed: August Job time : 995 secs
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                                                          316 TGTCAAAGACCATTGTGTCC
                                                                            1 TGTCAAAAACCGTTGTGTCC
                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-FEB-2000) Department of Microbiology, University of Hong Kong, Prince of Wales Hospital, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 450)
Chan, P.K.S., Lam, C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 450)
Chan, P.K.S., Lam, C.W., Li, W.H., Chan, M.Y.M., Cheung, J.L.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng, A.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           papillomavirus ty cancerous lesions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus typ
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inpublished
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                                                                                                                                                                                                      158
                                                                                                                         Conservative
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                                                                                                                                                                                                  /translation-"MFQDAEEKPRTLHDLCQALETSVHEIELKCVECKKTLQRSEVYD
FVFADLRIVYROGHFAYCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIR
CIICQRPLCPEKKRHVDLNKREHNISGRWTGRCAVCWRPRRRQTQV"
100 c 104 g 128 t
                                                                                                                                                                                                                                                                                                                                                                        /country="China"
/note="from cervical scrape of squamous cell carcinoma of the
                                                                                                                                                                                                                                                                                                                               p53-binding"
                                                                                                                                                                                                                                                               /codon_start=1
/product="E6 protein"
/protein_id="AAF60305.1"
/db_xref="GI:7331168"
                                                                                                                                                                                                                                                                                                                                          'note-"oncoprotein; transforming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Human papillomavirus type 58"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:10598"
                                                                                                                                                                                                                                                                                                                                                                                                                                      'isolate="QEH61"
             23,
                                                                                                                                      84.0%;
90.0%;
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s type 58
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cervix"
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                                                                                                                         0;
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Title: Perfect score: Sequence:

US-09-927-585A-1 20 1 tgtcaaaaaccgttg

tgtcaaaaaccgttgtgtcc

20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

2552756 seqs, 1349719017 residues

Run on: OM nucleic

.

nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

August 23, 2003, 05:06:07; Search time 206.5 Seconds (without alignments) 261.447 Million cell updates/sec

Minimum Maximum

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length:

2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 s

summaries

Database

N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/ger
2: /SIDS1/gcgdata/ger
3: /SIDS1/gcgdata/ger
4: /SIDS1/gcgdata/ger
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7: /SIDS1/gcgdata/ger

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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Description

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SUMMARIES

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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: *
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AAQ48566 AAS18612 ABZ75144 AAQ48556 AAQ48575 AAQ48560 ABT11435

ABS62861

Yeast sel Selected

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HPV E6/7 region pr
Middle-high hazard
Oncogenic HPV region pr
HPV E6/7 region pr
HPV E6/7 region pr
Yeast selected int
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                                                                                                                                                       Human papilloma virus; HPV; E6; E7; benign; malignant; probe; ss
                                                                                                           03-AUG-1993
                                                                                                                                         Synthetic
                                                                                                                                                                       HPV E6/7 region probe.
 Disclosure; Page 15; 18pp; Japanese
                                                                                             19-AUG-1991;
                                                                                                                           JP05192200-A
                        Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                                WPI; 1993-277497/35.
                                                              (TAKI ) TAKARA SHUZO
                                                                              20-AUG-1990;
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16
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ABL10478
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                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                              DNA encoding novel Human immune/haema HPV E6/7 region pr hPV Primer set 13, E6 oncogene from H HPV-PTM related ol Human papillomavir Human papillomavir Human bone marrow probe #105 for ge Human bone marrow probe #005 for ge Probe #006 used t Human liver single Human genome-deriv E6 SiRNA sequence. HPV16 E6 SiRNA sequence. HPV16 E6 SiRNA der Human papilloma vi Mammalian vestibul HPV16 E6 FFT encodi
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Aspergillus fumiga
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Aspergillus fumiga
Aspergillus fumiga
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Partial nucleotide
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Pyrococcus abyssi
DNA encoding novel
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                                                                                                        The invention describes a novel method of identifying viral DNA of human papilifomavirus (HPV) in cellular material collected from an individual. The method comprises extracting DNA from the cellular material, amplifying the DNA by using a polymerase, and identifying sequences complementary to sequences in the regions E (early genes) e.g. E6 and E7 cells is now based on identification of a nucleotide sequence in the L1 identify the presence of HPV virus in every stage of infection and to distinguish between virus strains having low hazard and virus strains region of middle-high hazard. This is the primer used to identify the E6 hazard and virus strains region of middle-high hazard HPV strains in infected cells, described in
                                                                                    Sequence
                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                     Identifying viral DNA of human papilloma virus in cellular material collected from an individual, by using polymerase and identifying sequences complementary to regions E of the viral genome using a
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-075253/10
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                                                                                                                                                                                                                                                                                                                                                                                                   (BIOA-) BIOANALISI CENT SUD DI PERSEU SINIBLADO
                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-2000; 2000IT-MO00091
                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-IB00771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus; HPV; early gene; E6; PCR primer; middle-high hazard; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Middle-high hazard human papillomavirus (HPV) E6, PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS18612 standard; DNA; 20 BP
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us. The probe binds
           1 TGTCAAAAACCGTTGTGTCC 20
                                       20;
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                                                 Similarity
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                                                                                                                                                                                                                                                                         Page 12; 17pp; English.
Similarity
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                                                                                    B₽;
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                                              100.0%;
                                                                                5 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect benign and/or malignant human papilloma
is to the E6 and/or E7 region of the virus.
                                                                                                                                                                                                                                                                                                                                                                                Floris MM;
                                   0;
                                                        Score
                                              Pred. No.
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                                  Mismatches
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The invention relates to a method for preparing a stabilised reaction CC mixture which contains at least one enzyme and which is at least CC matrially dried. The method involves removing the water from an aqueous reaction mixture containing an enzyme and a three-component stabiliser CC solution until the residual moisture content is 30% or less. The CC agent which protects against dessication, an inhibitor of condensation CC groups, and an inert polymer that forms a mesh structure that inhibits the method in the dried reactants. The dried reaction mixtures can be custed as "ready-to-use" mixtures for performing a wide range of nucleic cused as "ready-to-use" mixtures for performing a wide range of nucleic cused as "ready-to-use" mixtures for performing a wide range of nucleic cand/or restriction analysis, e.g., for the diagnostic detection of components needed to perform a particular reaction, hybridisation of components needed to perform a particular reaction, already deposited in reaction vessel, which eliminates the need for multiple additions consported and stored at ambient temperature without significant loss (amblify regions of human papillomavirus (HPV) genomes in order to camplify regions of human papillomavirus (HPV) genomes in order to characterise their type. Primers MaZ75142-MaZ75143 are PCR primers used to amplify a 450 bp region designated II which is shared by all HPV constants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stabilized reaction mixture containing an enzyme, useful for performing nucleic acid reactions, includes three-component stabilizing mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example VI; Page 41; 76pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Franco De Sarabia Rosado PM,
Marin Alberdi MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOT-) BIOTOOLS BIOTECHNOLOGICAL & MEDICAL LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2001; 2001ES-0000569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-2002;
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type 18.
type 31.
type 33.
type 35.
type 52b.
type 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Limones Lopez G, Madejon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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RESULT 5
AAQ48575
   RESULT 4
AAQ48556
ID AAQ4
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                                                                                                                                                                                                                                 SXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                          Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
           Synthetic
                            Human papilloma virus; HPV;
                                                                                                                                                                                                                                               The probe is used to detect benign and/or malignant human papilloma virus. The probe binds to the E6 and/or E7 region of the virus.
                                                                                                                                                                                                                                                                           Disclosure; Page 14; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                       Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma
                                               HPV E6/7 Genomic region.
                                                                   22-FEB-1994
                                                                                     AAQ48575;
                                                                                                       AAQ48575 standard; DNA; 1023 BP
                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      WPI; 1993-277497/35
                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                   JP05192200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papilloma virus; HPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPV E6/7 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ48556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ48556 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region designated E6-E7 from oncogenic HPV types
                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                           l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGTCAAAAACCGTTGTGTCC 20
||||||||||||||||||||||||||
1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 100.0%; Score 20; DB 25; Similarity 100.0%; Pred. No. 2.3; 20; Conservative 0; Mismatches 0,
                                                                                                                                                     TGTCAAAGACCGTTGTGTCC 20
                                                                                                                                                                TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                           Conservative
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                          90JP-0217067
                                                                                                                                                                                                                                                                                                                                                                                             91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 5 C; 4 G; 6 T; 0 other;
                                                                                                                                                                                                  92.0%;
                           benign; malignant;
                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6; E7; benign; malignant; probe; ss
                                                                                                                                                                                                  Score 18.4;
Pred. No. 14;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                            DB 14;
                                                                                                                                                                                         ļ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                             Ε6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                            Length
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                            E7;
                                                                                                                                                                                                            20;
                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                         0:
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                                                                                                                                                                                                                                                        RESULT 6
AAQ48560
밁
                                                                                                                                                                                                                                                                                                                                                                          SXCCCCXXX
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                   Probes
virus.
       Detecting benign and/or malignant human papilloma virus detecting DNA sequence of E6 and/or E7 region of human pap
                                    WPI; 1993-277497/35.
                                                                         20-AUG-1990;
                                                                                                               03-AUG-1993.
                                                                                                                                 JP05192200-A.
                                                                                                                                                   Synthetic.
                                                                                                                                                                     Human papilloma virus; HPV; E6;
                                                                                                                                                                                       HPV E6/7 region probe
                                                                                                                                                                                                            22-FEB-1994
                                                                                                                                                                                                                              AAQ48560;
                                                                                                                                                                                                                                                AAQ48560 standard;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1023 BP; 355 A; 170 C; 227 G;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 16-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting benign and/or malignant human papilloma virus - b detecting the DNA sequence of E6 and/or E7 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-277497/35.
P-PSDB; AAR40919, AAR48202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                      (TAKI ) TAKARA SHUZO CO
                                                                                            19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP05192200-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKI ) TAKARA SHUZO CO
                                                                                                                                                                                                                                                                                             1 TGTCAAAAACCGTTGTGTCC 20
|||||||||||||| |||||||
565 TGTCAAAAACCGCTGTGTCC 584
                                                                                                                                                                                                                                                                                                                                   l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   were designed to detect benign and/or malignant human papilloma The probes bind to the E6 and/or E7 region of human papilloma
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                         90JP-0217067
                                                                                            91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90JP-0217067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91JP-0230839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/label= ORF-1
/note= "E6 reg
702..998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 250..696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= ORF-2
/note= "E7 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                            92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٦
                                                                                                                                                                                                                                                20
                                                      LTD
                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region"
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                            Score 18.4;
Pred. No. 18
                                                                                                                                                                    E7; benign; malignant; probe;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                        271 T; 0 other;
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DB 14;

Length 1023; Indels

0;

Gaps

0

SS

ý papilloma

papilloma

밁

309

TGTGAAAAACCGTTGTTTCC

290

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RESULT 7
ABT11435/
ID ABT1
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                                   Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 18
                                                                                                                       The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RIM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present
                                                                                                                                                                                                                                                               drug screening or development, secretion yield of protein, or infection or cancer) -
                                                                                                                                                                                                                                                                        New protein-protein complexes of Saccharomyces cerevisiae, useful in drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast; protein-protein interaction; Selected Interacting Domain; SID (RTM); secretion yield; cancer; neurodegenerative disease; f cytostatic; neuroprotective; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The probe :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                     Sequence
                                                                                                                                                                                                                                      Claim 7; Page 168;
                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2001; 2001US-269266P
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2002; 2002WO-EP02299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200266504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast selected interacting domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT11435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABT11435
                                                                                                                                                                                                                                                                                                                                                                Legrain
                                                                                                                                                                                                                                                                                                                                                                                         (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2002
                                                                                                                                                                                                                                                                                                                            2002-674913/72.
DB; ABJ11118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                      l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                 ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCAAAAACCGTTGTGTCC 20
TGTCAAAAACCGTTGTGTCC
                                                                                                              is a coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 BP; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCAAAGACCTTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to
                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                    184 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 5 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                      357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detect benign and/or malignant human papilloma is to the E6 and/or E7 region of the virus.
                                                84.0%;
                                                                                                              sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
                                                                                     116 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                     0,
                                                Score 16.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 86;
                                                                                     113
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding sequence SEQ
                                                                                    <u>ن</u>
                                                                                     127
                                                  ,1e+02;
                                                            DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; fungicide;
                                                             540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                     Gaps
                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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RESULT 8
ABS62861/c
ID ABS62861 s
RESULT 9
AAH70910,
ID AAH7
XX AAH7
AC AAH7
XX 19-S
XX
DT 19-S
XX
DE Huma
XX
CETV
XX
OS Homc
XX
                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                         The invention relates to a complex between two interacting Saccharomyces cerevisiae polypeptides, comprising two Selected Interacting Domain (SID polypeptides as bait and prey proteins. A pharmaceutical composition comprising the complex is useful for preventing or treating Candida infection, cancer and neurodegenerative diseases in a human or animal, preferably in a mammal. This sequence represents DNA encoding a SID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New complex between two interacting bait and prey Saccharomyces cerevisiae polypeptides, useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; neuroprotective; Candida infection; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast; selected interacting
                                      Cervical cancer;
                                                                                                                                                                                                                                                                                                     Sequence 541 BP; 184 A; 116 C; 114 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 80; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-619165/66.
P-PSDB; ABG77247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200259255-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selected Interacting Domain (SID) polynucleotide #58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS62861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2001; 2001US-264577P
                                                               Human cervical
                                                                                        19-SEP-2001
                                                                                                                ААН70910;
                                                                                                                                        ААН70910
                                                                                                                                                                                                                                                                                                                             polypeptide
                                                                                                                                                                                                      310
                                                                                                                                                                                                                                                       l Similarity
18; Conserv
                                                                                                                                         standard;
                                                                                                                                                                                                      TGTGAAAAACCGTTGTTTCC 291
                                                                                                                                                                                                                             TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002WO-EP01350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                        (first
                                                              cancer marker nucleic acid 2184.
                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease.
                                                                                                                                        cDNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                  84.0%;
90.0%;
                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; SID; gene;
                                                                                                                                                                                                                                                       0;
                                      pre-malignant condition;
                                                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 1.
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                         127 T; 0 other;
                                                                                                                                                                                                                                                                    .1e+02
                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; antifungal; cancer;
                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                         Indels
                                      gene
                                        therapy;
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                       Gaps
                                        SS
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0;

WO200142467-A2

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RESULT 10
AAN91602
ID AAN91
XX AAN91
AC AAN91
XX 17-JU
DT 17-JU
DT 17-JU
DT 17-JU
OS Parti
DE type
XX Human
KW cellu
OS Human
XX W0890
XX W0890
XX W0890
XX W0890
XX W0890
XX W0890
XX WO890
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for infiniting cervical cancer in a patient. The nucleic acids may also be
                                           Schwartz DE,
                                                                                                                                 02-OCT-1987;
                                                                                                                                                                          30-SEP-1988;
                                                                                                                                                                                                                     06-APR-1989
                                                                                                                                                                                                                                                         WO8902934-A.
                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                  Human papilloma cellular smear;
                                                                                                                                                                                                                                                                                                                                                                                                                  Partial nucleotide sequence type 33 (HPV-33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN91602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 766 BP; 197 A; 158 C; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) cervical cancer with cytostatic activity. The nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN91602 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000;
12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001.
                                                                                      (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734
                                                                                                                                                                                                                                                                                                         papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 462; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US33312
                                           Adams
                                                                                                                               87US-0103979
                                                                                                                                                                          88WO-US03367
                                                                                                                                                                                                                                                                                                                                                virus; type 33; in cervical carcinoma
                                                                                                                                                                                                                                                                                                         virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>'5</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
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                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                      end) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao
                                                                                                                                                                                                                                                                                                                                                                       situ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                       hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                       assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with ids and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                           Query Match
Best Local S
                                                                       Matches
                                                                                                                                                                      The patent is for a rapid in situ hybridisation assay for detecting and typing human papilloma virus (HPV) in non-frozen cellular smears fixed t a support in absence of aldehyde-based crosslinking reagents. The assay comprises: (1) combining nucleic acid in the sample with at least one detectable probe able to hybridise with 1 or more HPV types; and (2) detecting presence or absence of hybrid complexes. Opt. several probes are used, eg one for HPV types 6 and 11, associated with benign warts, and one for types 16, 18, 31, 33 and 35, associated with cervical cancer. The assay can differentiate between HPV types. It is esp. used as a secondary test. The probes can be synthesised or cloned.
                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation test for human papilloma virus in cuby reaction with long labelled probe specific for virus types, esp. for examining cervical smears
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
1 TGTCAAAAACCGTTGTGTCC 20
                                                                     18; Conserv
                                                                                                                                         774 BP;
                                                                     Conservative
                                                                                                                                         270
                                                                                    84.0%;
90.0%;
                                                                                                                                       A; 132 C; 163 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                     0
                                                                                      Score 16.8;
Pred. No. 1
                                                                     Mismatches
                                                                                        .1e+02
                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                             cell smears
                                                                                                    Length
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                                                                       Indels
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RESULT 11
ABQ76303/c
                         vasotropic; vaccine
apoptosis; fungal;
neurodegeneration;
                                                                                                   S. cerevisiae
                                                                                                                                                                                     ABQ76303 standard;
Saccharomyces
                                                                                                                                21-NOV-2002
                                                                                                                                                           ABQ76303;
                                                                     Bax-resistance;
                                                         vaccine;
                                                                                                                             (first entry)
 cerevisiae.
                                                                                                   BAX-associated
                            yeast; infecell death;
                                                                                                                                                                                       CDNA;
                                                       cytostatic; fungicide; immunosuppressive; virucide; gene therapy; proliferative disorder; cancer;
                                                                                                                                                                                       3443
                                          infection;
                                                                                                   cDNA fragment SEQ
                                                                                                                                                                                       ВP
                                           autoimmune
                                                                                                   Ħ
                                          disease;
                                                                                                   31.
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443

<u>.</u>.

22-AUG-2002. WO200264766-A2

22-DEC-2000; 04-JAN-2001; 09-JAN-2001; ; 2000EP-0870318. ; 2001EP-0870002. ; 2001EP-0870003.

21-DEC-2001; 2001WO-EP15398

(JANC) JANSSEN PHARM ş

Contreras RH, Eberhardt ī, Luyten WHML, Reekmans ŖJ;

New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases 2002-667002/71. DB; ABG93037.

Claim 36; Figure 1; 344pp; English.

This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying. identifying

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RESULT 12
AAF25493/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida spp. sequences that are differentially expressed in a pathway ceventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the crivention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, and isolated nucleic acids, polypeptides, pharmaceutical compositions, and isolated nucleic acids, polypeptides, pharmaceutical compositions, are useful as medicaments or in creating a medicament for treating, preventing and/or alleviating creatises associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds creating a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fingal infections. Apoptosis related diseases include autoimmune disease, this sequence represents a polynucleotide associated with the Bax gene contents.
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Matches
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  The present
describes ad
                                                                                                        New polynucleotides encoding AMP deaminase or adenosine deaminase used e.g. for designing or identifying herbicides that inhibit the enzyme activities, and as probes for genetic or physical mapping -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF25493 standard; DNA; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                 Claim 2; Page 53; 72pp; English
                                                                                                                                                                                                                                                                    Caspar T,
                                                                                                                                                                                                                                                                                                              (PION-)
                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000WO-US21009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200109305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMP deaminase; adenosine deaminase; adenosine; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2001
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                                                                                                                                                                                                 2001-159866/16.
DB; AAB31953.
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                                                                                                                                                                                                                                                                                                              DU PONT DE NEMOURS
PIONEER HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                    Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  99US-0146473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202..312
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
  encodes a deaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%;
90.0%;
                                                                                                                                                                                                                                                                    Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a rice AMP deaminase enzyme.
                                                                                                                                                                                                                                                                                                              INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "AMP deaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                    an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8;
Pred. No. 1
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n AMP deaminase. The specification . These enzymes convert adenosine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                    Weng
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                                                                                                                                                                                                                                                                    Ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2e+02
                                                                                                                                                                                                                                                                    Hu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                       also
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adenosine

The present sequence encodes an andenosine deaminase. The specification also describes adenosine deaminase. These enzymes convert adenosine to

Claim 2;

Page 67-68; 72pp;

English

оř

also describes inosine. Mutati

Mutations in these

genes

cause disruptions in

then

salvage

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RESULT 13
AAF25498/c
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В
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deaminase and adenosine deaminase may be used to prepare antibodies to these proteins, and to design or identify herbicides that inhibit their enzyme activities. The polynucleotides are used as probes for genetically and physically mapping genes that they compose, and as markers for traits linked to those genes, where such information may be used in plant breeding to develop lines with desired phenotypes. The nucleic acid fragments may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species, and in polymerase chain reaction (PCR) protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. These may also be used to create transgenic plants in which the polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 530 BP; 156 A; 123 C; 98 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overexpressed or suppressed, and as probes in direct situ hybridisation ({\tt FISH}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inosine. Mutations in these genes cause disruptions in the catabolism of adenosine and AMP. In humans, this may lead
                                                                                activities, and as
                                                                                                                                                                            Caspar T,
                                                                                                                                                                                                                                              30-JUL-1999;
                                                                                                                                                                                                                                                                                                  08-FEB-2001.
                                                                                                                                                                                                                                                                                                                             WO200109305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP deaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF25498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF25498 standard; DNA; 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            white blood cells, which causes severe immunodeficiencies.
                                                                                            New polynucleotides encoding AMP deaminase or adenosine deaminase used e.g. for designing or identifying herbicides that inhibit the enzyme
                                                                                                                                                   WPI; 2001-159866/16.
                                                                                                                                                                                                                                                                         28-JUL-2000; 2000WO-US21009
                                                                                                                                      P-PSDB;
                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS (PION-) PIONEER HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    inosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
16; Conserv
                                                                                                                                      AAB31958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCAAAAACCGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCAAAAACCGTTGT 16
                                                                                                                                                                            Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenosine deaminase; adenosine; transgenic plant;
                                                                                                                                                                                                                                            99US-0146473
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 188..1255
                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "adenosine deaminase"
                                                                                                                                                                            SC,
                                                                               probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
                                                                                                                                                                            Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                       INI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soybean adenosine deaminase
                                                                                                                                                                                                      INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                               genetic
                                                                                                                                                                            Weng Z,
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hes 0;
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RESULT 14
AAH41227/
ID AAH4
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Matches 16
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The present invention relates to the genomic sequence of Pyrococcus abyss1 and P. abyss1 proteins (see AAB96053-AAB96842). P. abyss1 is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyss1. The 5' end of this sequence overlaps with the 3' end of AAH41226
                                                                                                                              Claim
                                                                                                                                                                  New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                       Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                               WPI; 2001-126236/14.
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Weissenbach
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/note= "This sequence overlaps with the
AAH41226"
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                                                                                                                                                                                                                                                                       Prieur D,
J, Saurin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperthermophilic protein;
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Pred. No.
                                                                                                                            French
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severe immunodeficiencies. The
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                                                                                                                                                                                       Pyrococcus
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2.8e+02;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABP4131-ABP55305), and also encompasses polypeptides 90% identical and polypucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polypucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polypucleotides and preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and

tumours of ovarian or

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RESULT
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ABQ55587/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disord infertility; pregnancy disorder; anovulation; polycystic ovary sypcos; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; chromosome mapping;
antibody preparation; cytostatic;
antiinflammatory; gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uses, since the proteins are stable at v 110 degrees centigrade. Note: This patent is in the same patent contains additional sequences as shown i AAH75903-AAH75920 and AAG66436.
                                                                                                                                                 Claim 1; SEQ ID No 1467; 2922pp; English.
                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                              WPI; 2002-147878/19
P-PSDB; ABP42510.
                                                                                                                                                                                                                                                                                      Birse CE,
                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2001; 2001WO-US18569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ55587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up
                                                                                                                                                                           neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2002
                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen HODFV22 cDNA, SEQ ID NO:1467.
                                                                                                                                                                                                                                                                                      CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulatory; neuroprotective;
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. 3.9e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
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Search completed: August 23, 2003, 10:38:17 Job time: 208.5 secs
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 611 BP; 212 A; 106 C; 120 G; 154 T; 19 other;
                                                                                                                                                                                291 GTCAAATACCTTTGTGTCC 273
                                                                                                                                                                                                                                2 GTCAAAAACCGTTGTGTCC 20
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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                            US-08-461-038-9
US-08-461-645-9
US-09-000-094-21
US-09-000-094-23
US-09-000-094-25
US-09-000-094-25
US-09-521-526-2
PCT-US95-11859-2
US-09-345-2368-76
US-09-345-2368-78
US-09-345-2368-79
US-08-487-283A-17
US-08-487-283A-11
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21, Appl
23, Appl
45, Appl
               1142,
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Appli
Appli
Query Match
Best Local Similarity
Thes 20; Conserve
                                                                         US-08-479-817-9
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US-08-479-817-9/c
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              100.0%; ilarity 100.0%; Conservative 0
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45	44	43	42	41	40	39	38	37	36	35	3 4	33	32	31	30	29	28
14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2
71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
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US-09-292-034-1	US-08-874-162-1	US-08-485-241-1	US-08-299-675-1	US-09-195-966-1	PCT-US94-05277-1	US-09-041-886-24	US-09-972-800A-1	US-09-087-465-1	PCT-US95-17025-3	US-08-956-653A-3	US-09-364-970-10	US-08-948-547-3	US-08-956-869-3	US-08-956-652-3	US-08-820-754-3	US-08-852-091-3	US-08-369-796-3
Sequence 1, Appli	Sequence 24, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 10, Appl	Sequence 3, Appli										

ALIGNMENTS

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APPLICATION NUMBER: US/08/307,026
FILING DATE:
APPLICATION NUMBER: US 07/805,537
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3440
REFERENCE (212) 840-0712
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08479817 Patent No. 5597910
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,817
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMATION: Gudibande, Satyanarayama APPLICANT: Gudibande, Satyanarayama APPLICANT: Kenten, John H.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: IMPROVED ELECTROCHEMI
TITLE OF INVENTION: FOR DNA PROBE ASSAYS
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
LENGTH: 30 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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CITY: New York
STATE: New York
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530 Fifth Avenue
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Score 20; DB 1; Pred. No. 0.051; ; Mismatches

DB 1; Length 30; 0

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US-08-461-645-9/c
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GENERAL INFORMATION:
                                                                                                                                                                      Sequence 9, Application Patent No. 5686244 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: EVAIN, BAILY
REGISTATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: INTITLE OF INVENTION: FO NUMBER OF SEQUENCES: 1
                                                                                                        APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: IMPROVED ELECTROCHEMILUMINESCENT LABEL
TITLE OF INVENTION: FOR DNA PROBE ASSAYS
                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/461,038 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   Local
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STATE: New York
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STATE:
              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                             STREET:
                                            ADDRESSEE:
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             New York
                                                                                                                                                                                                         Application US/08461645
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                               530 Fifth Avenue
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                                          Curtis, Morris & Safford
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212) 840-0712
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100.0%; Pred. No. 0.051;
tive 0; Mismatches
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US-09-000-094-19
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, BAITY
REGISTRATION NUMBER: 22,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                           EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTAATTCGGTGCTACCTG 10
                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLONEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCMILLAN, Nigel Alan John WILLIAMS, Mark Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARGETTS, Mary Brigid
COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holland
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INFORMATION
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Length 1128; Indels

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US-09-000-094-21
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Patent No. 6365160
GENERAL INFORMATION:
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                         COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/000,094

FILING DATE: 21-Apr-1998

CLASSIFICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 21-Apr-1996
APPLICATION NUMBER: WO PCT/AU96/00473

FILING DATE: 27-JUL-1996
APPLICATION NUMBER: AU PN 4439/95

FILING DATE: 27-JUL-1995
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 017227/0137

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5390

TELEFAX: (202) 672-5390
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1. 1104
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 TGCTAATTCGGTGCTACCTG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09000094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
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                 (202) 672-5300
02) 672-5399
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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US-09-000-094-23
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                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: CUNknown>
PRIOR APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
PREFERENCE TO COLUMN NUMBER: 21,7127
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les 20; Conserv
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..1125
SEQUENCE DESCRIPTION: SEQ ID
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LENGTH: 1128 base pairs
FEATURE:
                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
                                                ENCE CHARACTERISTICS:
LENGTH: 1398 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                           TELEFAX: (202)
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                 TYPE: DNA (genomic)
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WILLIAMS, Mark Philip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLONEY, Margaret Bridget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAZER, Ian
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                                                                                                                                               672-5399
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Pred. No. 0.082;
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RESULT 7
US-09-000-094-45
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                                                US-09-000-094-45
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application Patent No. 6365160
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 45:
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                         LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: -CURROWN->
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                           FEATURE:
                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                   LENGTH: 4770 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/AU96/00473 FILING DATE: 26-JUL-1996 APPLICATION NUMBER: AU PN 4439/95 FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                             NAME/KEY:
                                                                                                                                                                                                                                    TELEFAX: (202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
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OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
R OF SEQUENCES: 50
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1..1395
                                                                                                                          DNA (genomic)
                                                                                                                                       linear
                                                                                           CDS
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   100.0%;
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 Score
Pred.
                                                              ID NO:
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 No.
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   DB 4;
0.099;
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              Length 4770;
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                                                                                                                                                                 RESULT 9
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                                                                                                                   Sequence 2, Application PC/TUS9511859 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    Query Match
Best Local
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APPLICANT: JANSEN
APPLICANT: HOFMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1930
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                        APPLICANT: JANSEN, KATHRIN U. APPLICANT: HOFMANN, KATHRYN J. TITLE OF INVENTION: DNA ENCODING TITLE OF INVENTION: 6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 8010 base pairs
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ADDRESSEE: CHRISTINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC cc
OPERATING SYSTEM: F
SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2357 TGCTAATTCGGTGCTACCTG 2376
                                                                                                                                                                                                            401 TGCTAATTCGGTGCTACCTG 420
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HOFMANN, KATHRYN J.
   126
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                                                                                                                                                                                                                                                                        Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   linear
CHRISTINE E. CARTY
6 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [F]
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LINCOLN AVENUE -
                                                                                                                                                                                                                                                                      100.0%; S
100.0%; F
ative 0;
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ER: 19307
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                                                                                                                                                                                                                                                                                    Score 20; DB 3
Pred. No. 0.11;
                                                                                                                                                                                                                                                                         Mismatches
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                                                                           HUMAN PAPILLOMA VIRUS TYPE
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 P.O.
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BOX 2000
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RESULT 11
US-09-345-236B-76
; Sequence 76, Application US/09345236B
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-5
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US-09-228-986-5/c
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PCT-US95-11859-2
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09228986 Patent No. 6359198
                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the modification of PJ
FILE REFERENCE: 11000/1020
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT: FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE_DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 07065-0907
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
TWPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/11859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                            1176 GCTAATTCGTTGCTACC 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                              2 GCTAATTCGGTGCTACC 18
                                                                                                                                                                 l Similarity
16; Conserv
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                                                                                                                                                                                 77.0%;
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Pred. No. 31;
0; Mismatches
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Query Match
Best Local Similarity
Matches 16; Conserve
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                                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(165)
US-09-345-236B-78
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APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, 1
TITLE OF INVENTION: Compositions, and Methods for
TILE REFERENCE: 21042_0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-345-236B-78
                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 78 LENGTH: 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 76 LENGTH: 692
                                                               Matches
                                                                                            Query Match
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CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
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TITLE OF INVENTION: No. 6521454el Baculoviruses, I
TITLE OF INVENTION: Compositions, and Methods for
FILE REFERENCE: 21042.0004
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Becnel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                 LENGTH: 692
TYPE: DNA
ORGANISM: mosquito baculovirus
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                                                                              Match 74.0%;
Local Similarity 88.9%;
 165
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3 CTAATTCGGTGCTACCTG
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                                                               16;
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White, Susan E.
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                                                               Conservative
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Pred. No. 5
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Pred. No. 5
                                                               Mismatches
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RESULT 13 US-09-345-236B-80/c ; Sequence 80, Application US/09345236B ; Patent No. 6521454

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(366)
; NAME/KEY: CDS
; LOCATION: (529)...(690)
US-09-345-236B-80
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US--,
EARLIER APPLICATION NUMBER: PCT/US--,
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
TILING DATE: 1997-03-07
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APPLICANT: Undeen, Albert H.

TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REPERENCE: 21042-0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 692
TYPET: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: mosquito baculovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80,
642052
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                                         APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633
                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/
FILING DATE: 1997-03-07
                                                                                                     FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,597
                                                                                                                                                                                  APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
                                                                                                                                                                                                                             APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/040,626 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,583 FILING DATE: 1997-05-23
                                                                                         FILING DATE: 1997-05-23
                                                                                                                                     APPLICATION NUMBER: 60/047,615
                                                                                                                                                       FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/040,334
                              FILING DATE: 1997-05-
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                FILING DATE: 1997-03-07
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: Tukuo, Fukuda
: Moser, Bettina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 Human Secreted proteins
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88.9%;
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Pred.
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No. 54
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EARLIER APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23 FILING DATE: 1997-05-APPLICATION NUMBER: 6
FILING DATE: 1997-05-APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,580 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 FILING DATE: 1997-05-APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-APPLICATION NUMBER: APPLICATION NUMBER: 60/047,581 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 FILING DATE: APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-04-13 FILING DATE: 1997-04-1 FILING DATE: 1997-04-APPLICATION NUMBER: FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-APPLICATION NUMBER: APPLICATION FILING DATE: 1997-06-06 60/043,568 60/047,582 60/047,492 60/056,893 60/056,886 60/047,596 60/056,878 60/056,630 60/043,569 60/047,598 60/047,584 60/047,618

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APPLICATION NUMBER: 1997-05-23
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APPLICATION NUMBER: 60/056,911
APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/043,576
APPLICATION NUMBER: 60/043,576
                                                                     APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578
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                                                                                                                                                                                                                                                  FILING DATE:
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FILING DATE: 1997-05-23
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APPLICANT: DUFF, GORDON W.
APPLICANT: COX, ANGELA
APPLICANT: COX, NICOLA J.
APPLICANT: DIGIOVINE, FRANCESCO S.
APPLICANT: DIGIOVINE, FRANCESCO S.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
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CURRENT APPLICATION NUMBER: US/09/345,217
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: PCT/GB98/01481
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ER FILLING DATE: 1997-06-06
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clade; Panicoideae; Andropogoneae; Zea.
        Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                          Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 4
                                                                             Unpublished
                                                                                    Sequencing of the maize genome
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Yu, Y., Kim, H.R., Hat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicots; core eudicots; asterids; lamiids; Solanales; Bolanaceae; Solanum; Lycopersicon. 1 (bases 1 to 370)
1 (bases 1 to 370)
1 (bases 1, Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13r
Class: BAC ends.
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Plate: 15 row:
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100 Jordan Hall, Clemson, SC
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                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished Contact: CU
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon
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/note="Vector: pBeloBAC1; Site_1: HindIII;
HindIII; Zea mays L. ssp. mays"
145 c 178 g 286 t 1 others
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                                                  /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoL; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4578"
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/lab_host="DH10B"
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                  locules were discarded prior to freezing the 77\ c 79\ g 107\ t
                                                                                                                              /clone_lib="tomato breaker fruit, TIGR"
                                                                                                                                             /lab_host="SOLR"
                                                                                                                                                                /tissue_type="Pericarp"
/dev_stage="breaker"
                                                                                                                                                                                                   /db_xref="taxon:4081"
/clone="cLEG33L22"
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sequence.
AL290320
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GSS; genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 528)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                                                    Tetraodon nigroviridis genome surve
109D19 of library G from Tetraodon
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                                                                                                                                                                                                                                                                     /note="Organ: sperm;
E-Coli DH10B"
150 c 114 g
                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/mol_type-"genomic DNA"
/mol_type-"genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2252 Co1=12 Row-C"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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Adams,M.D.
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Submitted (12-APR-2000) Genoscope - Centre National of Submitted (12-APR-2000) Genoscope - Centre National of Submitted (12-APR-2000) Genoscope - FRANCE (E-mail: seqref@gel-wab : www.genoscope.cns.fr)

This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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MDL.46E23.SP6 Notre Dame Liverpool
NDL.46E23, genomic survey sequence.
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CC122092.1 GI:29991147
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                   Other_GSSs: NDL.46E23.T7
                                     Unpublished
                                                                                                                                      Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
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 Contact: Brendan Loftus
                                               1 (bases 1 to 600)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/mal_type="genomic DNA"
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/clone="109D19"
                                                                                                 Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Genoscope sequence ID
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Email: enta@tigr.org
Library was provided be
Seg primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                    Email: enta@tigr.org
Library was provided
Seg primer: SP6
                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive,
Tel: 301-838-3543
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Other_GSSs: NDL.91K13.T7
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Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
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Aedes aegypti
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan
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/clone="WDL.46E23"
/clone="WDL.46E23"
/clone="Lib="Notre Dame Liverpool"
/clone="Vector: pECBAC1; Site_1: Hind III; The library for the prepared from whole body tissue of newly hatched L1 by David Severson at the University of Notre Dame and Hongbin Zhang"
a 160 c 181 g 79 t
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/note="Vector: pBCBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
108 c 240 g 167 t
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/strain="Liverpool"
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/mol_type="genomic DNA"
/strain="Liverpool"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loftus, B., Shetty, \hat{J}., Knudson, D. and BAC end sequencing of Aedes aegypti Unpublished
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1 (bases 1 to 932)
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/mol_type-"genomic DNA"
/strain-"Liverpool"
/db_xref-"taxon:7159"
/clone-"NDL.91B22"
                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and
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Endopterygota; Diptera; Nematocera; Culicoidea; Aec
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1 (bases 1 to 226)

Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishii, Y., Itoh; M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Romura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Romura, K., Sasaki, D., Sato, K., Shibata, Y., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Naramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

Y and Hayashizki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho, Tsurumi-ku, Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           visit our web site (http://genome.rtc.riken.go.jp) for
                     3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk exc
from Lambda FLC I"
56 c 52 g 55 t
                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGAFCCAACAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                         prepared by using trehalose thermo-activated reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="skin"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 0 day neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="4633401D12"
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                                                                                                                excision
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TGCTAATTCGGTGCTACCT

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RESULT 9
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                                                                                                                                                                                                      44
               AU114943 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk723hl 3', mRNA sequence.
AU114943
AU114943.1 GI:10928510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mccomble@cshl.org
Plate: hs83 row: c colu
Seq primer: -21Ml3UnivFwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Marttenssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH878622 273 bp DNA linear GSS 05-AUG-
hs83c03.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hs83c03 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
                                                                                                 AU114943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 273.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was dispested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "
a 58 c 47 g 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="hs83c03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
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                                                                                                                                                                                                                                                                                                       79.0%;
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                                                                                                                                                                                                                                                                                      Score 15.8; DB 28;
Pred. No. 1.7e+03;
0; Mismatches 2;
                                                                                              300 bp
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                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH397091 376 bp DNA linear AG-ND-168H24.TF ND-TAM Anopheles gambiae genomic c , genomic survey sequence.
BH397091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 300)
                                                                    Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain
                                                                                                                                                                                                                                    Construction of a BAC library and generation of BAC sequence-tayged connectors for genome sequencing of malaria mosquito Anopheles gambiae Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                                                                                                                                                                                                                           Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4
                                                                                                                                                                                   Other_GSSs: AG-ND-168H24.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH397091.1 GI:17343307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A complementary view of the C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y
                                                                                                                                                                                                    12655398
                                                                                                                                                                                                                                                                                                              and Collins, F.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTAATTCGGTGCTACCT 19
                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 376)
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                                                   bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="varied"
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/clone="yk723h1"
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Pred. No. 1.7e+03;
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one AG-ND-168H24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 bp ig01c01.b1 WGS-ZmaysF (DH5a methyl 1g01c01, genomic survey sequence. CC159313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCTAATTCGGTGCTACCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Katzenburger, F., King, L., Miller, B., Muller, S., Zutavern, T., McCombie, W.R. and Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                              High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Class: shotgun
                                                                                                                                                                                                                                                                                                                                            Plate: ig01 row: c colu
Seq primer: -21M13UnivFwd
                                                                                                                                                                                                                                                                                                                                                                                  Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: W. Richard McCombie
Lita Annenberg Hazen Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic shotgun sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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17; Conservative
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/clone="AG-ND-168H24"
/clone_lib="ND-TAM"
/note="Vector: pEcBAC1;
a 75 c 101 g
/Glone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic
/strain="PEST"
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                                                                                                                                                                         /db_xref="taxon:4577"
                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Anopheles gambiae"
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                                                                                                                                  /lab_host="DH5a"
                                                                                                                                                          /clone="ig01c01"
                                                                                                                                                                                                                                         organism="Zea mays"
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89.5%;
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Zea mays (methyl-filtered)
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92 t
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RESULT 13
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                                                     Query Match
Best Local S
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Best Local :
                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GCAAATTCAGTGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                        (web address: www.rzpd.de)
Seq primer: T3 ET from Amersham
Seq primer: T4 ecquence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., J., S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Undd., K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter, Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterstoned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 bp mRNA linear EST 13-FEI fm62g01.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone IMAGE:4200001 5', mRNA sequence.
Ŋ
                                    Similarity 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: zbrafishewatson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Centes
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Evatihopterygil; Neopterygil; Teleostel; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 427)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
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                                                                                                                           'dev_stage="1-2 years"

/lab_host="E.Coli XLI-Blue MRF' (XLI-Blue MRF')"

/clone_lib="Zebrafish adult retina cDNA"

/note="Vector: Lambda ZAP II (pBluescript SK-);

ECORI; Site_2: SalI; This Zebrafish library was

constructed by Dr. Susan E. Brockerhoff (email:

sbrocker@u.washington.edu) RZPD library number:

a 106 c 97 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19,..b/g reads in pUC19). The same ligation was transformed into DH5a."

73 c 72 g 127 t
                                                                                                                                                                                                                                                                                              /strain="wild-type"
/db_xref="taxon:7955"
/clone="IMAGE:4200001"
                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                              /sex="mixed"
                                                       79.0%;
89.5%;
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Pred. No. 1.9e+03
20
                                                     Score 15.8;
Pred. No. 1.
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                                                         .9e+03;
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                                    0;
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GCTAATTCAGTGCTAGCTG

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RESULT 15
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MEDLINE
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Best Local
      AUTHORS
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AQ678663.1
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RC2-UT0087-200900-110-h04
BQ378925
BQ378925.1 GI:21054439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCTAATTCGGTGCTACCT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2094 row: L column: 20 Seq primer: M13 Reverse Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ678663 470 bp DNA HS_2094_B2_F10_MR CIT Approved Human Gen sapiens genomic clone Plate=2094 Col=20
      Dias
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 523)
                                                                                                                              Homo sapiens
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Location/Qualifiers
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1 (bases 1 to 470)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and Mahairas,G.G., Wallace,J.C., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G.C., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Mahairas,G.G., Wallace,G.C., Wallace,
                                                                                                                                                            Homo sapiens (human)
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1 100 c 79 q 168 +
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Search completed: August 23, Job time : 1852 secs
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seq primer: puc 18 forward
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High quality sequence stop: 523
Location/Qualifiers
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Fax: +55-11-2707001
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Ludwig Institute for Cancer Re
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/mol_type="mRNA"
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/dev_stage="Adult"
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Maximum DB seq length: 2000000000
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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49, 1		Sequence 252550,			Sequence 160032,		202	Sequence 83, Appl	16, /	71:	۲,		Sequence 1, Appli	71	Sequence 3, Appli	Sequence 316, App	Sequence 264047,		Sequence 216899,				Sequence 243504,	Sequence 12873, A	Sequence 262303,	Sequence 165367,	Sequence 198644,	Sequence 198643,

; NUMBER OF SEQ ID NOS: 3 ; SOFTWARE: FastSEQ for W ; SEO ID NO 74539 ; LENGTH: 427 ; TYPE: DNA ; ORGANISM: Human US-10-027-632-74539 RESULT 1 US-10-027-632-74539 ; Sequence 74539, Application US/10027632 ; GENERAL INFORMATION: ; APPLICANT: Wang, David G. ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide ; TITLE OF INVENTION: Polymorphisms in the Human Genome 밁 Q Query Match Best Local Similarity Matches 17; Conserv CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR FILING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23 FILE REFERENCE: 108827.129 276 GYTAATTCGGTGCTATCTG 294 2 GCTAATTCGGTGCTACCTG 20 |:|||||||||||||| Conservative for Windows Version 4.0 325720 85.0%; 89.5%; 1; Score 17; Pred. No. Mismatches 13; 1; Length 427; Indels 0; Gaps

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14 US-10-079-854-249
14 US-10-074-095-928
9 US-09-764-878-36
9 US-09-764-860-170
14 US-10-079-854-36
4 US-10-074-095-170
2 US-10-128-714-257
2 US-10-101-464A-5
3 US-10-027-632-35375
US-10-027-632-60413
US-10-027-632-60413

Sequence 249, App Sequence 228, App Sequence 249, App Sequence 36, Appl Sequence 36, Appl Sequence 170, Appl Sequence 170, Appl Sequence 257, Appl Sequence 19, Appl Sequence 752, Appl Sequence 752, Appl Sequence 35375, Appl Sequence 60413, A

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Sequence 74539, A

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; ORGANISM: Homo sapiens
US-09-764-878-249
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; ORGANISM: Homo sapiens
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                                                                                 Sequence 249, Application US/10079854
Publication No. US20030054368A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
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APPLICANT: Rosen et
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Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 249
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                           Matches
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CURRENT FILING DATE: 2001-01-17
                                                  Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198 SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Nuc
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                                 SOFTWARE: PatentIn Ver.
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1
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CURRENT FILING DATE: 2002-02-14
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-06-28
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FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
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APPLICATION NUMBER: 60/216,880
FILING DATE: 2000-07-07
APPLICATION NUMBER: 60/225,270
FILING DATE: 2000-08-14
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                                                          FILING DATE: 2000-08-APPLICATION NUMBER: 6
FILING DATE: 2000-09-
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FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
FILING DATE: 2000-09-27
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DR APPLICATION NUMBER: 60/229,343
DR FILING DATE: 2000-09-01
DR APPLICATION NUMBER: 60/229,345
DR FILING DATE: 2000-09-01
DR APPLICATION NUMBER: 60/229,287
DR FILING DATE: 2000-09-01
DR APPLICATION NUMBER: 60/229,513
DR APPLICATION NUMBER: 60/231,413
DR FILING DATE: 2000-09-08
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DR FILING DATE: 2000-09-08
DR APPLICATION NUMBER: 60/231,509
DR APPLICATION NUMBER: 60/236,367
DR APPLICATION NUMBER: 60/237,039
DR FILING DATE: 2000-10-09-29
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DR FILING DATE: 2000-10-02
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DR APPLICATION NUMBER: 60/236,370

APPLICATION NUMBER: 60/237,037 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,040

APPLICATION NUMBER: 60/ FILING DATE: 2000-10-02

NUMBER: 60/236,802

FILING DATE:

E: 2000-10-02

N NUMBER: 60/237,038

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N NUMBER: 60/236,370

N NUMBER: 60/236,370

OR APPLICATION NUMBER: 60/225,268
OR FILING DATE: 2000-08-14
OR PAPPLICATION NUMBER: 60/236,368
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/251,856
OR FILING DATE: 2000-12-08
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/251,868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/229,344

FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01

FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327

NUMBER: 60/241,809

FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
FILING DATE: 2000-09-25

Query Match Best Local S Matches 17 17; Conservative 79.0%; 89.5%; Score 15.8; DB 14; Pred. No. 1e+02; 0; Mismatches 2; Length Indels 281; 0 Gaps

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DR FILING DATE: 2000-10-02

PR APPLICATION NUMBER: 60/240,960

PR FILING DATE: 2000-10-20

PR APPLICATION NUMBER: 60/239,935

PR APPLICATION NUMBER: 60/239,935

PR APPLICATION NUMBER: 60/241,787

PR FILING DATE: 2000-10-13

PR APPLICATION NUMBER: 60/246,474

PR FILING DATE: 2000-11-08

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PR FILING DATE: 2000-11-08

PR APPLICATION NUMBER: 60/246,532

PR FILING DATE: 2000-11-17

PR APPLICATION NUMBER: 60/249,216

PR APPLICATION NUMBER: 60/249,216

PR APPLICATION NUMBER: 60/229,210

PR APPLICATION NUMBER: 60/225,681

PR APPLICATION NUMBER: 60/225,759

PR APPLICATION NUMBER: 60/225,718

PR APPLICATION NUMBER: 60/227,182

PR APPLICATION NUMBER: 60/227,182

PR APPLICATION NUMBER: 60/225,213

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US-09-764-860-170
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US-09-764-878-36
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                                                                                                                                                                                                                                                                   SOFTWARE: Pat
SEQ ID NO 170
LENGTH: 287
TYPE: DNA
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Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
Sequence
                                                                                                                                                    Query Match
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,860 CURRENT FILING DATE: 2001-01-17
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NUMBER OF SEQ ID NOS: 1198
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LOCATION: (1)
OTHER INFORMATION: n equals a,t,g,
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b. US20020090615A1
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; LOCATION: (1) ; OTHER INFORMATION: n equals a,t,g, or US-10-079-854-36
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Matches 17
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
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CURRENT FILING DATE: 2002-02-22
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CURRENT FILING DATE: 2002-02-14
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC008C1
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NAME/KEY: misc_feature
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TYPE: DNA
ORGANISM: Homo sapiens
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                                  APPLICATION NUMBER: 60/216,880 FILING DATE: 2000-07-07
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FILING DATE: 2000-08-14
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 FILING DATE:
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OR FILING DATE: 2000-09-27

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OR APPLICATION NUMBER: 60/234,223

OR FILING DATE: 2000-09-21

OR APPLICATION NUMBER: 60/224,924

OR APPLICATION NUMBER: 60/224,518

OR FILING DATE: 2000-08-14

OR FILING DATE: 2000-08-14

APPLICATION NUMBER: 60/235,834 FILING DATE: 2000-09-27

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32, 32, 32, 32,	249, 244 249, 217 249, 211 249, 215 249, 264 249, 214 249, 297 232, 400 232, 081 232, 081	7235, 836 7230, 438 7230, 438 7215, 135 7215, 266 7249, 218 7249, 208 7249, 208 7249, 213 7249, 213 7249, 213 7249, 207 7249, 213	249 249 225 225 227

OR APPLICATION NUMBER: 60/236, 369
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/220, 964
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/24, 809
OR FILING DATE: 2000-010-20
OR APPLICATION NUMBER: 60/24, 809
OR FILING DATE: 2000-10-17
OR APPLICATION NUMBER: 60/24, 809
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OR APPLICATION NUMBER: 60/24, 817
OR APPLICATION NUMBER: 60/24, 817
OR APPLICATION NUMBER: 60/24, 817
OR APPLICATION NUMBER: 60/25, 268
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/25, 868
OR FILING DATE: 2000-09-12
OR APPLICATION NUMBER: 60/25, 868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/25, 868
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OR APPLICATION NUMBER: 60/25, 868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/25, 868
OR FILING DATE: 2000-09-25
OR APPLICATION NUMBER: 60/23, 344
OR APPLICATION NUMBER: 60/23, 345
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RESULT 11
US-10-295-362-19/c
; Sequence 19, Application US/10295362
; Publication No. US20030143745A1
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US-10-128-714-257/c
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APPLICANT: Hu, Wer
APPLICANT: Tishkoi
APPLICANT: Zamudi
APPLICANT: Eroshk
APPLICANT: Lemieux
                                                      GENERAL INFORMATION:
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TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-06-05
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APPLICANT: Aventis Pharma
APPLICANT: Martinez, Asu
APPLICANT: Kolvek, Steve
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
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Tishkoff, Daniel
Zamudio, Carlos
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Pred. No. 1.4e
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US-10-044-090-752; Sequence 752, Application No. US20; GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 14468
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Best Local (
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Expressing and Assay FILE REFERENCE: USAV2001/0145 PCT CURRENT APPLICATION NUMBER: US/10/295,362 CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILLING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 00/162,866
PRIOR FILLING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 0071620000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/335,181 PRIOR FILING DATE: 2001-11-15 NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genetically Modified Bacterial Strains and No. US20030143745A1 TITLE OF INVENTION: Expressing and Assaying Natural Products
                APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/00724 PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                              Local
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  APPLICATION
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16; Conserv
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                                                                                             Application US/10044090 o. US20020137081A1
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NUMBER: US/10/044,090
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Pred. No. 1
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Pred. No. 2.
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; LENGTH: 457
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-35375
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US-10-027-632-60413
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US-10-027-632-35375/c
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 034851.1
US-10-044-090-752
              Sequence 60413, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827-1970/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
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NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 752
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Best Local 9
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
OR FILING DATE: 1999-09-28
OR FILING DATE: 1999-09-28
OR FILING DATE: 1999-09-09
OR FILING DATE: 1999-09-09
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APPLICATION NUMBER: US 60/218,006
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17; Conservative
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Pred. No. 2.1e
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Pred. No. 2.3e+02;
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Query Match
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                                                                                                                                                                                                            SOFTWARE: Fast
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                           ENGTH: 457
418 TGCTAATTCTCTGCTACATG 437
                                 1 TGCTAATTCGGTGCTACCTG 20
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Search completed: August 23, 2003, 13:53:17 Job time : $142\ secs$

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Perfect score:
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 00000 Score Query Match 000 290670 348250 165468 173316 231561 238650 242958 242958 245636 252185 192687 198067 213001 214621 223389 466 667 168268 298050 147349 Length 1751 2065 2443 7916 28939 34216 34589 AC112011 AC1229871 AC122980 AC121043 AP003592 0 ALB07796 AL935260 AC131316 BX530057 AC118630 AC118630 AC118630 AC108412 AF255339 PPHE6E AF092932 HPU40822 AF436130 AC129311 AC141726 AL731823 AC135943 1 PAPA6B AR169144 ALIGNMENTS ARI16914 Sequence L41216 Human papil AF602932 Human papil AF436130 Human papil AC141726 Apis mell AL731823 Mouse DNA AC135943 Rattus no AC012980 Rattus no AC012980 Rattus no AC0298071 Rattus no AC0298072 Rattus no AC0298070 Rattus no AC0121043 Rattus no AC0121043 Rattus no AC0121043 Rattus no AC0121043 Rattus no AC0123050 Nostoc sp AL807796 Mouse DNA AL935260 Lactobaci AP005800 Oryza satt AC0131316 Mus muscu AC124524 Mus muscu AC124524 Mus muscu AC108412 Mus muscu AC108414 Ac1d1thio X57036 Bacteriopha AX301236 Sequence E05232 Part of DNA E05256 Primer for I34500 Sequence 9 I73213 Sequence 9 AF126428 Human pap AR202651 Sequence AR202652 Sequence AR202671 Sequence AR202671 Sequence AR20203 Genital hum AC112240 Homo sapi AC024790 Caenorhab AJ006589 Bacteriop U31784 Human papil AL391808 Human DNA U57054 Caenorhabdi BC044687 Xenopus 1 AB017002 Dugesia j Description

20 bp	DNA
from Patent W00185994.	
GI:17382323	
construct construct sequences.	
de Montis, A. and Floris, M.M.	`X

RESULT 1
AX301236
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Sequence 5: Ax301236 Ax301236.1

from

linear

PAT 30-NOV-2001

AX301236

Bioanalisi	Patent: WO	Method and	Perseu,S.,	1	•		
Centro Sud S.N.C. Di Perseu Siniblado EC. (0185994-A 5 15-NOV-2001;	means for identifying hpv virus	de Montis, A. and Floris, M.M.		sequences.	construct	construct

IT)

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE ORGANISM

Pred.

No.

51

the number of results predicted by chance to have

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JOBP
JOF Human papillc.

-/3422

-A/2.

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E05256
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20
Primer for amplifying Human
R05256
E05256.1 GI:2173446
JP 1993192200-A/26.
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19-AUG-1991 JP 1991230839
20-AUG-1990 JP 90P 217067
OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN,
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer representative of region E6 of
HPV virus having low oncogenic hazard"
1 5 c 5 g 7 t
                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630" 7 t
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                                                                          PAT 29-SEP-1997
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FUKUSHIMA MICHIO,
PI FUJINAGA KEI
PC C120,170, C120,
CC strandedness:
CC topology: Lin
CC hypothetical:
CC anti-sense: N
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I34500
Sequence
I57335
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Gudibande, S.R. and Kenten, J.H.
Electrochemiluminescent label for DNA
Patent: US 5597910-A 9 28-JAN-1997;
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1 (Dases 1 to 20)
Chazawa,K., Shimada,M., Katou,I., Fukushima,M.
DETECTION OF HIMAN PAPILLOMA VIRUS
Patent: JP 1993192200-A 26 03-AUG-1993;
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synthetic construct
artificial sequences.
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strandedness: Single;
topology: Linear;
hypothetical: NO;
anti-sense: NO.
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Artificial sequence; Genes.
JP 1993192200-A/26
03-AUG-1993
19-AUG-1991 JP 1991230839
20-AUG-1990 JP 90P 217067
20-AUG-1990 JP 90P 217067
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                         PAT 07-OCT-1997
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VERSION
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DEFINITION
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AF126428
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          J. Virol.
99214361
             Ai,W., Toussaint,E. and Roman,A.

CCAAT displacement protein binds to and negatively papillomavirus type 6 E6, E7, and E1 promoters J. Virol. 73 (5), 4220-4229 (1999)
                                                                            Human papillomavirus type 6
Human papillomavirus type 6
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                           _
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 30) Gudibande, S.R. and Kenten, J.H. Method for detecting a nucleic acid analyte using an electrochemiluminescent label Patent: US 5686244-A 9 11-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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Gudibande, S. R. and Kenten, J. H.
Method for conducting a polymerase chain
electrochemiluminescent label
Patent: US 5610017-A 9 11-MAR-1997;
                                                                                                                                 Human papillomavirus type AF126428
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 from 173213
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Similarity 100.0%;
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Unclassified.
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Sequence
AR202652
                                                                                                                                                  1 TGCTAATTCGGTGCTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
AR202651
Unknown
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Submitted (05-FEB-1999) Microbiology and Immunology,
University School of Medicine, 635 Barnhill Drive, It
46202-5120, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 697) Ai, W. and Roman, A.
          Unknown.
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llarity 100.0%;
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/product="E6 protein"
/product="E6 protein"
/protein_id="AAD29398.1"
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RCYLCHKPLCEVEKVKHILTKARFIKLNCTWKGRCLHCWTTCMEDMLP"
144 c 145 g 175 t
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                                                                                                                                                                                                                                                       /organism="unknown"
269 c 213 g
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/mol_type="genomic DNA"
/strain="W50"
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BASE COUNT
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AUTHORS
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AR202671
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FEATURES
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AUTHORS
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AR202653
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Sequence 23
AR202653
AR202653.1
                                                                                                                                                                                    Sequence
AR202671
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                                                                                                                                                                                                                                                                                                                                                                                                               Webb, E.Ann., Margetts, M.Brigid., Cox, J.Cooper., McMillan, N.Alan.John., Williams, M.Philip., Moloney, M.Bridget.Holland. and Edwards, S.John. Papillomavirus polyprotein constructs Patent: US 6365160-A 23 02-APR-2002;
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                                                       1 (bases 1 to 4770)
Webb, E. Ann., Margetts, M. Brigid., Cox, J. Cooper., McMillan, N. Alan. John., Williams, M. Philip., McMillan, M. Bridget. Holland. and Edwards, S. John. Papillomavirus polyprotein constructs Patent: US 6365160-A 45 02-APR-2002;
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275 c 240 g
          /organism="unknown"
890 c 1071 a
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331 c 283 g
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1 TGCTAATTCGGTGCTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwarz,E., Durst,M., Demankowski,C., Lattermann,O., Zech,R., Wolfsperger,E., Suhai,S. and zur Hausen,H.

DNA sequence and genome organization of genital human papillomavirus type 6b

EMBO J. 2 (12), 2341-2348 (1983)
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El gene; E2 gene; E4 gene; E5a gene; E5b gene; E6 gene; gene; L2 gene; major capsid protein L1; minor capsid proregulatory protein E2; replication protein E1.
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Genital human papillomavirus type 6b (HPV6b).
X00203
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                                                           832. .2781
/gene="E1"
832. .2781
                                                                                                                                                                                                                                                                                         /gene="1530..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT: D06462"
/translation="MESANASTSATTIDQLCKTFNLSMHTLQINCVFCKNALTTAEIY
/translation="MESANASTSATTIDQLCKTFNLSMHTLQINCVFCKNALTTAEIY
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832 . 2781
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/protein_id="CAA25018.1"
/db_xref="GI:60956"
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/strain="type 6b (HPV6b)"
/db_xref="taxon:10600"
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                                          'gene="El"
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protein

E1,

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FWLQPLVDAKVALLDDATQPCWIYMTYMRNILDGNPMSIDRKHKALTLIKCPPLLVT
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4159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="E5a"
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2723. .3829
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                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                     'gene="E5b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation-"MGAPNIGKYVMAAQLYVLLHLYLALHKKYPFLNLLHTPPHRPPP
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ORIGIN
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FEATURES
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AR169144
LOCUS
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Mismatches

Indels

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Gaps

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Sequence 2 from patent US 6290965.
AR169144
20; Conserv
                                                                                                                                                          DNA encoding human papillomavirus type Patent: US 6290965-A 2 18-SEP-2001; Location/Qualifiers
                                                                                                                                                                                                                      Unclassified.
1 (bases 1 to 8010)
Jansen, K.U. and Hofmann, K.J.
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100.0%; ilarity 100.0%; Conservative 0.
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1527 c 1718 g
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7316. .7339
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SSELDQYPLGKFLLQSGYRGRSSIRTGVKRPAVSKASAAPKRKRAKTKR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDIIRLHRPAIASRRGLVRYSRIGQRGSMHTRSGKHIGARIHYFYDISPIAQAAEEIE
MHPLVAAQDDTFDIYAESFEPGINPTQHPVTNISDTYLTSTPNTVTQPWGNTTVPLSL
PNDLFLQSGPDITFPTAPWGTPFSPVTPALPTGPVFITGSGFYLHPAWYFARKRRKRI
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                                                                                                                                             .8010
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100.0%; Pred. No.
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                   Score 20;
Pred. No.
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                   DB 6;
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                                      Length 8010;
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El gene; E2 gene; E4 gene; E5 gene; E6 gene; E7 gene; L
gene; complete genome.
Human papillomavirus type 6a
Human papillomavirus type 6a
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hofmann, K.J., Cook, J.C., Joyce, J.G., Brown, D.R., Schultz, L.D., George, H.A., Rosolowsky, M., Fife, K. H. and Jansen, K. U. Sequence determination of human papillomavirus type 6a and assembly of virus-like particles in Saccharomyces cerevisiae virus-graphy 209 (2), 506-518 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10, 1995 this sequence version replaced gi:790893. al source text: Human papillomavirus type 6a DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-
531. .
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103. .555
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833. .835 is first start codon; putative"
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103. .
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531. .533 is first start codon; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCYLCHKPLCEVEKVKHILTKARFIKLNCTWKGRCLHCWTTCMEDMLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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103. .105 is first
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                                                                                                                                                                            /codon_start=1
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lrst start codon; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon;
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                                                                                                                                                                                                                       CDS
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EVGRGQPLGVGVSGHPFLNKYDDVENSGSGGNPGQDNRVNVGMDYKQTQLCMVGCAPP
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/gene="E4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="E2"
2724. .383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIEFIPFLSKFKLWLHGTPKKNCIAIVGPPDTGKSYFCMSLISFLGGTVISHVNSSSH
FWLQPLVDAKVALLDDATQPCWIYMDTYMRNLLDGNPMSIDRKHKALTLIKCPPLLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIVSLIEESAIINAGAPEIVPPAHGGFTITSSETTTPAILDVSVTSHTTTSIFRNPVF
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RPRVGLYSRALHQVQVTDPAFLSTPQRLITYDNPVYEGEDVSVQFSHDSIHNAPDEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEAIAKRLDACQEQLLELYEENSTDLNKHVLHWKCMRHESVLLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position 3286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTPVSSSTQEDAVQTPPRKRARGVQQSPCNALCVAHIGPVDSGNHNLITNNHDQHQR
RNNSNSSATPIVQFQGESNCLKCFRYRLNDKHRHLFDLISSTWHWASPKAPHKHAIVT
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                                                                                                                                                                                                                                    /note="base 5679
position 5790. .5
                                                                                                                                                                                                                                                                                                                                                                                                                  PLFFSDVAA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDIIRLHRPAIASRRGLYRYSRIGQRGSMHTRSGKHIGARIHYFYDISPIAQAAEEIE
MHPLVAAQDDTFDIYAESFEPDINPTQHPVTNISDTYLTSTPNTVTQPWGNTTVPLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  position 4424.
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                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                          PNDLFLOSGPDITFPTAPMGTPFSPVTPALPTGPVFITGSGFYLHPAWYFARKRRKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="base 4379 is f
position 4424. .4426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="E4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                    79 is first base .5792 is first s
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6 is first start codon; p
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start c
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                                                                                                                                                                                                                                    codon;
putative"
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GNRTSVGSSIYVNTPSGSLVSSEAQLFNKPYWLQKAQGHNNGICWGNQLFVTVVDTTR

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PUBMED
REFERENCE
AUTHORS
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AF092932
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ORGANISM
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ORIGIN
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JOURNAL
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MEDLINE
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Best Local
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                                                                                     Sg
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Human
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Human papillomavirus type 6, complete genome.
AF092932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kovelman.R., Bilter,G.K., Roman,A., Brown,D.R. and Barbosa,M.S. Human papillomavirus type 6: Classification of clinical isolates and functional analysis of E2 proteins
J. Gen. Virol. 80 (Pt 9), 2445-2451 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-SEP-1998) Virology, Signal Pharmaceuticals, 5555 Oberlin Drive, San Diego, CA 92121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses;
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VLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTPEKEKPDPYKNLSFWEVNLKEKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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gene

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gene CDS

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2724. .3830
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Search completed: August 23, 2003, 11:11:37 Job time: 997 secs
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78 a 1526 c 1713 g 2295 t
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PLFFSDVAA"
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                                                            JOURNAL
MEDLINE
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COMMENT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BM076659
LOCUS
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AUTHORS
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaea; Hypocrea.

1 (bases 1 to 670)
Chambergo,F.S., Bonaccorsi,E.D., Ferreira,A.J.S., Ramos,A.S.P.,
Ferreira,J.R.Jr., Abrahao-Neto,J., Farah,J.P.S. and El-Dorry,H.
Elucidation of the metabolic fate of glucose in the filamentous
fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
                       Contact: El-Dorry, Hamza
Department of Biochemistry
Institute of Chemistry. University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo,
                                                                                                                                                                                                                                                                                   BM076659
Trest-A0592
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ291095 629 bp DNA linear GSS 0: nbxb0038C14r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0038C14r, genomic surve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: Universal M13 forward primer BACKWARD: Universal M13 reverse primer Plate: 7 row: B column: 4
Seq primer: M13 reverse primer
                                                                                                                                                                                                                                                                                                                        Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

[] (bases 1 to 629)
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                                                                                                                                      High quality sequence stop: 481.
Location/Qualifiers
                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wing,R.A. and Dean,R.A.

BAC End Sequencing Framework to Sequence the Rice Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ291095.1 GI:3952385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Sex="Asexual
/tissue_type="Mycelia"
/dev_stage="18 hr Glycerol-grown culture"
/lab_host="E. coli SOLR cells (kanamycin resistant)"
/clone_lib="TrEST-A"
/clone="Wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/clone_lib="TrEST-A"
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                                                                                                                                                                                                                  BAC ends
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
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Pred. No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                              On Jan 28, 2002 this sequence version replaced gi:7709240 Contact: Arcaro MA, Morley M, Burdick J, Cheung VG Department of Pediatrics University of Pennsylvania 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UP_309-16G_SP6 RPCIll Human Male BAC Library Homo sapiens clone 309-16G, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheung, V.G., Dalrymple, H.L., Narasimhan, S., Watts, J., Schuler, G., Raap, A.K., Morley, M. and Bruzel, A.
A resource of mapped human bacterial artificial chromosome clones Genome Res. 9 (10), 989-993 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                   Tel: 215 590 2664
Fax: 215 590 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 831)
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                                                                                                                                         Seq primer: SP6
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                                                                                                                                                                                           Email: mlennox@mail.med.upenn.edu
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                                                                                                                     BAC ends
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                          1. .831
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/lab_host="E. coli DH10B"
                                                                                              Location/Qualifiers
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 190genic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be
                                                                          560 TGTCAAAWACTGTTGTGTC 578
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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR20D02 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR20D02"
/clone_lib="RPCI-98"
/note="end : TET3"
a 155 c 91 g 7;
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/clone_lib="RPCI11 Human Male BAC Library"
/note="Vector: pBACe3.6; RPCI11 Human Male BAC Library"
/ 189 c 174 g 242 t
                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster'
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                                                                                                                                                                        85.0%;
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100.0%;
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RESULT 6
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Tingey,S.V., Poweli,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished
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                                                                                                                                                    Triticum aestivum (bread wheat)
Triticum aestivum
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18; Conserv
                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
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5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
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Fax: 6179750995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished
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Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.Coli xhl.Blue mrf'"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
ECORI; Site_2: xho; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with xhoI,
for directional cloning into pre-digested lambda ZAP
Express vector. "
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/mol_type="mRNA"
/db_xref="taxon:7955"
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Ostariophysi; Cypriniform
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30 TGTCAAAAAACCATTGTTTCC 11
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Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished Other_ESTs: fv39c12.yl
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370 bp mRNA linear EST 21-NOV-200 fv39c12.xl Sugano SJD adult male Danio rerio cDNA clone IMAGE:5410942 3' similar to SW:RPA5_HUMAN 015160 DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE ;, mRNA sequence.
                                                                                                                                                                              Consortium/LLNL, send email to: info@
Trace considered overall poor quality
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
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1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
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                                                                                                                                                                                                                                                                                                   Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone
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Accinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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                         /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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/mol_type="mRNA"
/db_xref="taxon:4565"
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/clone="IMAGE:5410942"
                                                                                                                                                                                                                                          information can be found through the I LNL, send email to: info@image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritter, E.
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BE760467/c
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Best Local
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200 TGTCAAAAACCGTTGGGGCC 181
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1455 deMalsonneuve Blvd. West, Montreal, Quebec, CANADA, H3G 1M8
Tel: 514-848-3405
Fax: 514-848-4504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 bp mRNA linear EST 2. an_1726 Aspergillus niger, pYES2 (XhoI-EcoRI) Aspergillus cDNA clone 1726 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsang,A. and Storms,R. Aspergillus niger Expr Unpublished
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Aspergillus niger
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BACKWARD: GGCGTGAATGTAAGCGTGACATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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/lab_host="bH10B (phage resistant)"

/clone_lib="Sugano SJD adult male"

/clone_lib="Sugano SJD adult male"

/clone_lib="Sugano SJD adult male"

/note="Yector: pME18S-FL3; Site_1: DraIII (CACCATGTG);

Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CGACCTGCAGCTCGAACACCTGCG and 3' end primer

CGACCTGCAGCTCGAACACCACA. "82 * 14.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tsang@vax2.concordia.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 410
/Glone_lib="Aspergillus niger, pyES2 (XhoI-EcoRI)"
/Glone_lib="Aspergillus niger, pyES2 (XhoI-EcoRI)"
/note="Yector: pyES2; Site_1: Xho-I; Site_2: EcoRI; cDNA
was synthesized with Zap kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pyES2 (Invitrogen Corp). This vector
permits expression of our library in yeast. "
                                                                                                                                                                                                                                                                                  /organism="Aspergillus niger"
/mol_type="mRNA"
/db_xref="taxon:5061"
/clone="1726"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                           /lab_host="E. coli"
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/tissue_type="whole body"
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Pred. No. 4
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4e+02;
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SOURCE
ORGANISM
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BM201540
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| |||||||| |||||||||
70 TATCAAAAACAGTTGTGTCC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 bp mRNA linear EST 30-JAN-20 C0227A12-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone C0227A12 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: C0227 row: A column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A. and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mmalia; Eutheria; (bases 1 to 425)
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primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
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           5'-pGACTAGTTGTAGATCGCGACCGCCCTTTTTTTTTTTT-3'] from
7' ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sal1 and NotI enzymes
and cloned into Sal1/NotI site of pSPORT1 plasmid vector.
                                                                                                                                                                                                  /note="Vector: psport1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lqsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of four embryos at 7.5-days postcoltum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                         /tlssue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="niaEST:C0227A12-3"
/db_xref="taxon:10090"
/clone="C0227A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
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DH10B E. coli host was transformed with the ligation
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90.0%;
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Pred. No. 4.
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ches 2;
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                 RESULT 11
AI443887
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234 TGTCAAAAACCCTTTTGTCC 253
                                    1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence scanning the human genome
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Keller,A., Shaker,R., Furlong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 473
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TGTCAAAAACCATAGTGTCC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ing the human genome Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jwallace@u.washington.edu
                                                                                                                                                                    /Clone_lib="CIT Approved Human Genomic Sperm Library /note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones i E-Coli DH108"
101 c 88 g 126 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Tagged Connector
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/mol_type="senomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2020 Col=6 Row=K"
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g,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  approach to mapping and
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Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
Glycine max (soybean)
Glycine max
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Gm-c1004-2180 5' similar to TR:Q96502 Q96502 COL2. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,R., Waterston,R. and Wilso
Public Soybean EST Project
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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Fax: 314 286 1810
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                                        CDNA. First Strand Synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAGAGTCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EccAT adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cONA inserts. Blue colonies 9n=15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. 520-523-1372 (Virginia H. Coryell), Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the
520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
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/lab_host="XL10-Gold"
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Beck,C.,
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Mammalia; Eutheria; Primates;
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BASE COUNT
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584 TGTCAAAATCTGTTGTGTCC
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                                   BI830009
603080272F1 NIH_MGC_119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2602
              mRNA sequence.
BI830009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tingey,S.V., Powell,W., Wolters,P., Miao,G., Caraher,N. and Hanafey,M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
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BI830009.1 GI:15941559
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DuPont Wheat cDNA Sequence
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Scott. V. Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                        XhoI; Wheat (Triticum aestivum L.) root;
wrel library"
                                                                                                                                                                                                                                                                                                    /clone="wre1n.pk0094.c4"
/tlssue_type="root"
/clone_lb="wre1n"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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                                                                                                                                                                                                  Score 16.8;
Pred. No. 4
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No. 4.
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                                         sapiens cDNA clone IMAGE:5171968 5',
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Craniata; Vertebrata; Catarrhini; Hominidae

Euteleostomi;

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RESULT 14
BU941677
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AUTHORS
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AUTHORS
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Best Local
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1 (bases 1 to 875)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                           875 bp
AGENCOURT_10554416 NIH_MGC_127 H
IMAGE:6713986 5', mRNA sequence
BU941677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11427 row: p column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                          CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov c column: 10
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BU941677.1
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                             Jnpublished
                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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               quality sequence stop: 302
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/db_xref="taxon:9606"
/clone="IMAGE:5171968"
/tissue_type="medulla"
/lab_host="DH10B"
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Pred. No. 4.5e+02;
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Query Match
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                                                                                                                                                                                                      Plate: LLCM1219 row: 1 column: High quality sequence start: 2 High quality sequence stop: 686.
                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 929)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG335280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library."
193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH_MGC_128). Library creater ... ... Usdin, M.D., Ph.D. (NIMH, NIH). Note: this
                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4541350"
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/lab_host="DH10B (T1:phage-resistant)"
/clone_lib="NIH_MGC_127"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
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/mol_type="mRNA"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                 Location/Qualifiers
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90.0%;
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Pred. No. 4.8e+02;
D; Mismatches 2;
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BASE COUNT
ORIGIN
Search completed: August 23, 2003, 12:13:20 Job time: 1851 secs
                                                                                                                                                                                                                             Query Match 84.0%; Score 16.8; DB 10; Length 929; Best Local Similarity 90.0%; Pred. No. 4.8e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                           /clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
: /cgn2_6/ptodata/1/pubpna/USO9D_PUBCOMB.seq:*
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US-10-128-714-6427
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Sequence 34048, A	25869,	Sequence 25868, A		1753,	e 8841		õ	е 1	'n	۲,	'n	Sequence 1, Appl1	26	13	Sequence 5, Appli	9	ω	Sequence 3, Appli		Sequence 191550,	Sequence 71, Appl	Sequence 184710,	Sequence 10792, A	Sequence 6139, Ap

ALIGNMENTS

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US-10-286-387-8
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Publication No. US20030143529A1

GENERAL INFORMATION:
APPLICANT: Cytyc Corporation

TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes

FILE REFERENCE: cym-035CP

CURRENT APPLICATION NUMBER: US/10/286,387

CURRENT FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 8

LENGTH: 20
Sequence 18, Application US/10292848
Publication No. US20030119042A1
GENERAL INFORMATION:
APPLICANT: ROSADO, Pedro M.
APPLICANT: LOPEZ, Genma L.
APPLICANT: SEIZ, Antonio M.
APPLICANT: SEIZ, Antonio M.
APPLICANT: ALBERDI, Maria D.
APPLICANT: ALBERDI, Method for preparing stabilized reaction mixtures, which are t
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Best Local (
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ORGANISM: Artificial
FEATURE:
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Pred. No. 0.73;
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             NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENCTH: 23
TYPE: DNA
                                                                                                                                                                            Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 23
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Best Local (
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                                                                                             APPLICANT: Cytyc Corporation
TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
FILE REFERENCE: cym-035CP
CURRENT APPLICATION NUMBER: US/10/286,387
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes FILE REFERENCE: cyym-035CP CURRENT APPLICATION NUMBER: US/10/286,387 CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/ES02/00109
PRIOR FILING DATE: 2002-3-11
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ORGANISM: Artificial
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, OTHER INFORMATION: Forward primer used to amplify region of E6 US-10-286-387-10 \,
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SOFTWARE: Pate
SEQ ID NO 2427
LENGTH: 1409
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 23
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
FILE REFERNCE: Cym-035CP
CURRENT APPLICATION NUMBER: US/10/286,387
CURRENT FILING DATE: 2003-02-28
                                                                                            PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Methods of Use FILE REFERENCE: 10182-018-999
                                                                               PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                 PatentIn version
                                                                                                                                                                                                                                                                                                                                     Hu, Wenqi
Tishkoff, Daniel
Zamudio, Carlos
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Lemieux, Sebastien M
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No. US20030143529A1
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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenq1
APPLICANT: Hishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
CURRENT FILING DATE: 2002-04-26
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US-10-128-714-6427/c
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US-10-128-714-7427/c
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-7427
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR PRICING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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Best Local
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Best Local
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
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APPLICANT: Hu, Wengi
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PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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    APPLICATION NUMBER: US 60/285,697 FILING DATE: 2001-04-23
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l Similarity . 89.5%;
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RESULT 10

US-10-128-714-5427/c

; Sequence 5427, Application US/10128714

; Publication No. US20030119013A1

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; SEQ ID NO 6427
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-6427
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: Sequence 1427, Application US/10128714

: Publication No. US20030119013A1
                                                                                                                                                                                 SOFTWARE: Pater
SEQ ID NO 1427
LENGTH: 1521
TYPE: DNA
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
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Best Local
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Best Local :
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff Daniel
APPLICANT: Zamudio, Carlos
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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878 GCCAAAAACCCTTGTGTCC
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Pred. No. 2.2e+02
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Best Local Similarity
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                                               ; ORGANISM: Aspergillus fumigatus US-10-128-714-427
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US-10-128-714-427/c
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                         SOFTWARE: Pate
SEQ ID NO 427
LENGTH: 3520
TYPE: DNA
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SEQ ID NO 5427
LENGTH: 3518
      Query Match
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APPLICANT: LemiLeux, Sebastian M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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ITILE OF INVENTION: Methods of Use
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Tishkoff, Daniel
Zamudio, Carlos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eroshkin, Alexey M
Lemieux, Sebastien M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zamudio, Carlos
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                                                                                                                                                                                  NOS:
                                                                                                                                                           version 3.1
                                                                                                                                                                                                    2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.0%;
    79.0%;
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0; Mismatches
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    Score 15.8;
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    DB
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    14;
Length 3520;
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US-10-286-387-15
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: Cytyc Corporation
                                                                                        SOFTWARE: Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No.
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mansfield, Gary S.
TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE
TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-
FILE REFERENCE: A31304-BAE (072874.0156)
CURRENT APPLICATION NUMBER: US/09/941,492
CURRENT FILING DATE: 2002-04-01
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/133,717 PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/158,863 PRIOR FILING DATE: 1998-09-23
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/756,096 PRIOR FILING DATE: 2001-01-08
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/838,858 PRIOR FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Puttaraju, Madalah
APPLICANT: Mansfield, Gary S.
                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mitchell,
                 ORGANISM: Artificial Sequence FEATURE:
                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Binding domain of human papilloma virus PTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                APPLICATION NUMBER: 08/766,354
                                                                                                                                                                                   FILING DATE: 1998-05-28
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                                                                                                              FastSEQ for Windows Version
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No. US20030143529A1
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Pred. No. 2
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US-09-918-995-33830/c
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                                                                                                             GENERAL INFORMATION:
APPLICANT: HYSEG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-011-20
PRIOR FILING DATE: 1999-011-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Fas
SEQ ID NO 122
LENGTH: 138
                                                          NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33830
                                                                                                                                                                                                                                                                                                     Sequence 33830, Application US/09918995 Publication No. US20030073623A1
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Best Local :
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/756,096
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/158,863
PRIOR FILING DATE: 1998-09-23
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APPLICANT: Mansfield, Gary S.
TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE IN
TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-SPLICING
FILE REFERENCE: A31304-BAE (072874.0156)
CURRENT APPLICATION NUMBER: US/09/941,492
CURRENT FILING DATE: 2002-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/087,233
FILING DATE: 1998-05-28
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FILING DATE: 1998-08-13
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1 Similarity 85.0%;
17; Conservation
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85.0%;
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Pred. No. 2.9e+02;
O: Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 3.1e+02;
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US-09-918-995-33830
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Query Match
Best Local Similarity
Matches 17; Conserv
  Conservative
            76.0%;
85.0%;
Score 15.2; DB 11; Pred. No. 3.7e+02; 0; Mismatches 3;
                     Length 431;
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Search completed: August 23, 2003, 13:53:16 Job time : 147 secs

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /ggn2_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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    tgtcaaaaaccgttgtgtcc
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    Length
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US-09-359-382-11
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US-08-495-743-27/c
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US-09-000-094-21	US-09-000-094-19	US-09-477-135A-69	US-08-990-823-69	US-09-531-857A-1	US-09-080-044-1	US-09-560-579A-1	US-08-929-140-1	US-08-410-005-1	US-08-316-239B-2	US-08-316-239B-1	US-08-468-057A-9	US-08-074-879-9	US-08-332-638-41	US-08-188-228-41	US-08-819-177-2	US-08-332-638-53	US-08-332-643-47
Sequence 21, Appl	Sequence 19, Appl	Sequence 69, Appl	Sequence 69, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 41, Appl	Sequence 41, Appl	Sequence 2, Appli	Sequence 53, Appl	Sequence 47, Appl				

ALIGNMENTS

; ORIGINAL SOURCE: Synthetically prepared	
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ICAL: NO	
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: STRANDEDNESS: Single	
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; INFORMATION FOR SEQ ID NO: 27:	
477-4646	
; TELEPHONE: (716) 722-9332	
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; REFERENCE/DOCKET NUMBER: 67271A	
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; NAME: Tucker, J. Lanny	
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; APPLICATION NUMBER: US 08/062,023	
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; FILING DATE: 08-JUN-1995	
; APPLICATION NUMBER: US/08/495,743	
LICATION DATA:	
Word for Windows)	
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; MEDIUM TYPE: Diskette, 3.5inch, 1.44 MB storage (IBM)	
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Rochester	
State Street	
ADDRESSEE: Eastman Kodak Company, Patent Legal Staff	
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R OF SEQUENCES: 65	
OF INVENTION: HAVING MATCHED MELTIN	
OF INVENTION: OR MORE TARGET DNA'S USING PRI	
OF INVENTION:	
OF INVENTION:	
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; APPLICANT: John W.H. Sutherland, JoAnne H. Kerschner	
; APPLICANT: Thomas J. Cummins, Susan M. Atwood	
; GENERAL INFORMATION:	
; Sequence 27, Application US/08495743	
US-08-495-743-27/c	

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Query Match
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US-08-495-739-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                             NAME: Tucker, J. Lanny
REGISTATION NUMBER: 27,678
REFERENCE/DOCKET NUMBER: 67:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 722-9332
                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-D
SOFTWARE: PC-8 (Word f
CURRENT APPLICATION DATA:
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                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
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CLASSIFICATION: 435
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TOPOLOGY: Lir
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                                                          Local
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Lynn Bergmeyer, John B. Findlay
John W.H. Sutherland, Johnne H. Kerschner
TVENTION: DIAGNOSTIC COMPOSITIONS, ELEMENT
VENTION: METHODS AND TEST KITS FOR
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                                                                                                                                                                                                 Primer for hPV DNA
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                                                         76.0%;
85.0%;
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Sequence 27, Application US/08062023 Patent No. 6174668
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APPLICANT:
                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44
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                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Tucker, J. Lanny REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0: FILING DATE: 08-JUN-1995
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IRY: U.S.A.
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343 State Street
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John W.H. Sutherland, Joanne H. Kerschner
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                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                        Primer for hPV DNA
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                                                                                                                                                                                                                                               Synthetically prepared 
Same
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                                                                                                                                                                   76.0%;
85.0%;
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Pred. No. 36;
0; Mismatches
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GENERAL INFORMATION:

APPLICANT:

Thomas

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Cummins, Susan M.

Atwood

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Best Local Similarity. 85.0
                                                                                                                                                                                                             Patent No. 6287569
                                                                                                                                                                                            GENERAL INFORMATION:
                               CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
                                                                                                     TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING FILE REFERENCE: 233/221
                                                                                                                                                       APPLICANT: KIPPS, THO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPA: (716) 477-4646
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 29 nucleotides
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REFERENCE/DOCKET NUMBER: 67271A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 722-9332
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM: MS-
SOFTWARE: PC-8 (Word
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                  SEQ ID NOS:
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343 State Street
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for Windows Version 3.0
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W.H. Sutherland, JoAnne H. Kerschner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Lanny
                                                                                                                                                                                                                                                                                                                                                                                                          76.0%;
85.0%;
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Pred. No. 3
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LENGTH:
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Best Local Similarity
Matches 17; Conserv
                                                                                                     SEQ ID NO 11
LENGTH: 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                    APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
FULL REFERENCE: 17227/130
FULL REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 600455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/430,201
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,495
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eckert, Richard L.
APPLICANT: Crish, James F.
TITLE OF INVENTION: Tissue Specific Promoters and Transgenic Animals
TITLE OF INVENTION: the Screening of Pharmaceuticals
FILE REFERENCE: CASE-04022
                                                                                                                                 EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                          APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper
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                                                                                    TYPE: DNA
          NAME/KEY: CDS
LOCATION: (1)..(516)
                                                                ORGANISM: Artificial Sequence
FEATURE:
                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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Pred. No. 51;
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Pred. No. 51;
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Query Match Best Local :

Similarity

76.0%;

Score 15.2; Pred. No. 52;

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Length 525; Indels

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Pred. No. 52;); Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(516)
US-09-359-382-11
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SEQ ID NO 11
LENGTH: 519
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Best Local
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                                                                           SEQ ID NO 71
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TYPE: DNA
ORGANISM: Drosophila
-09-669-751-71
                                                                                                                                                                                                      APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Motion Sickness, Vertigo and Other Digarder of INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P-NI 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Appl
Patent No. 630639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/359,382 CURRENT FILING DATE: 1999-07-23 EARLIER APPLICATION NUMBER: US 08/860,165 EARLIER FILING DATE: 1997-09-22 EARLIER APPLICATION NUMBER: PCTAU95/00868 EARLIER FILING DATE: 1995-12-20
                                                                                                              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-12-02 NUMBER OF SEQ ID NOS: 261
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/669,751
CURRENT FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                         LENGTH:
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                                                                                              FastSEQ for Windows Version 4.0
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Pred. No. 52;
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Pred. No. 5
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                                Matches
                                                           Query Match
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TELEFAX: 708/948-2642
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Apple Macintosh System 7.0 SOFTWARE: Macintosh Text File CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      ANTI-SENSE: no ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                     TUPULUE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: May 6, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BA
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 44
                                                                                                                                                     AUTHORS: Section AUTHORS: Suhai, S., and authors: Suhai, S., and authors: Human Papillomavirus
                                              Local Similarity
                                                                                                         PAGES: 181-185
DATE: 1985
                                                                                                                                       VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple M
                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Baxter Diagnostics Inc.
STREET: One Baxter Parkway, Building DP-3E
CITY: Deerfield
                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                            NAME/KEY: Portion of viral genome coding
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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   1 TGTCAAAAACCGTTGTGTCC 20
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Mark Buonaiuto
Mark Buonaiuto
11,593
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                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                Seedorf, K., Krammer, G., Suhai, S., and Rowekamp,
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                                Conservative
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85.0%;
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                                             Score 15.2;
Pred. No. 53;
                                                                                                                                                                                    Type 16 DNA Sequence
                                Mismatches
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                                                            Length 570;
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APPLICANT:

PAUL V.

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RESULT 12
US-08-216-233C-1
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GENERAL INFORMATION:
APPLICANT: Janice T. Brown
             Sequence 1, Application US/08216233C Patent No. 5506105
                                                                                                                                                                Matches
                                                                                                                                                                                           Query Match
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mark Buonaluto
REGISTRAIN NUMBER: 31,593
REFERENCE/DOCKET NUMBER: BA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/948-2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
ADDRESSE: PACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: May 6, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Macintosh Te
                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                             Local
                                                                                                                                                                                                                                      PAGES: 181-185
DATE: 1985
                                                                                                                                                                                                                                                                                 JOURNAL: V1:
VOLUME: 145
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: dou
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple M
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                      338 TGTCAAAAGCCACTGTGTCC 357
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                                                                                                                                                             l Similarity
17; Conserv
                                                                                                                       1 TGTCAAAAACCGTTGTGTCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                             Subai, S., and Rowekamp, W.
Human Papillomavirus Type 16 DNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
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One Baxter Parkway, Building DP-3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708/948-2642
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                            Seedorf, K.,
                                                                                                                                                                                                                                                                                                                                                                       Portion of viral genome coding for E6/E7 polypeptides
                                                                                                                                                                                                                                                                                               Virology
                                                                                                                                                                                                                                                                                                                                                                                                                   Papaoviridae, Human papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no
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                                                                                                                                                                             76.0%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                         Krammer, G.,
                                                                                                                                                             0;
                                                                                                                                                                           Score 15.2;
Pred. No. 5
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                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                            Durst, M.,
                                                                                                                                                                                           BB
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                                                                                                                                                                                         Length 570;
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; OTHER INFORMATION: E6/E7-HPV16
US-09-210-168-3
                                                                                         SEQ ID NO 3
LENGTH: 779
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Lorincz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%;
Best Local Similarity 85.0%;
Matchés 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09210168 Patent No. 6355424
                                                                                                                                                      PRIOR FILING DATE: 1998-01-05
PRIOR PRICATION NUMBER: U.S. 60/069,426
PRIOR APPLICATION NUMBER: U.S. 60/069,426
PRIOR FILING DATE: 1997-12-12
NUMBER OF CENTE NOTE:
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/210,168 CURRENT FILING DATE: 1998-12-11 PRIOR APPLICATION NUMBER: U.S. 60/082,167 PRIOR EILING DATE: 1998-04-17 PRIOR APPLICATION NUMBER: U.S. 60/070,486 PRIOR FILING DATE: 1998-01-05
                                                                                                                               SOFTWARE:
                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (305) 222-66 INFORMATION FOR SEQ ID NO:
                                    TYPE: DNA
ORGANISM: Human papillomavirus
                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 34,745
TELECOMMUNICATION INFORMATION:
TELEPHONE: (305) 222-6423
TELEPAX: (305) 272-675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 776 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,456
FILING DATE: 10-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: TYMESON, CYNTHIA G. REGISTRATION NUMBER: 34,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                             PatentIn Ver. 2.1
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1717 DEERFIELD ROAD
                                                                                                                                                                                                                                                                                                              ON: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE 26294005US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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Pred. No. 5
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                                                                                                                              RESULT 15
US-08-860-165-9
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US-08-117-083-7
             Sequence 9, Application US/08860165A Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper APPLICANT: WEBB, Elizabeth Ann APPLICANT: FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 base pairs
TUDE: 1910-1916-1916
                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Bourso
APPLICANT: Inglis
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus
TITLE OF INVENTION: Papilloma Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-SEP CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                           342 TGTCAAAAGCCACTGTGTCC 361
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344 TGTCAAAAGCCACTGTGTCC 363
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17; Conserv
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                       linear
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85.0%;
                                                                                                                                                                                                                                                                                  76.0%;
85.0%;
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                                                                                                                                                                                                                                                                  Score 15.2; D
Pred. No. 55;
0; Mismatches
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Pred. No. 55;
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Matches
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                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1994-12-20 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)..(798)
                                                                                                                                                                                                                            LENGTH: 801
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                               FEATURE:
                                                                Local Similarity hes 17; Conserv
337 TGTCAAAAGCCACTGTGTCC 356
                1 TGTCAAAAACCGTTGTGTCC 20
                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.0
                                                                  Conservative
                                                                               76.0%;
85.0%;
                                                                0; Mismatches
                                                                               Score 15.2;
Pred. No. 55;
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                                                                                             Length 801;
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Search completed: August 23, 2003, 12:15:08 Job time : 51 secs